

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:38:10 ; Search time 10.8696 Seconds
(without alignments)
540.807 Million cell updates/sec

Title: US-09-147-443D-58
Perfect score: 669
Sequence: 1 QVTLSSGGVVGPGSLRV.....SRNYTMDVWGKGTVTSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	70.3	121	1 HV3J_HUMAN	P01771 homo sapien
2	460.5	68.8	122	1 HV3G_HUMAN	P01768 homo sapien
3	433.5	64.8	136	1 HV16_MOUSE	P01783 mus musculu
4	428.5	64.1	126	1 HV3K_HUMAN	P01772 homo sapien
5	417	62.3	119	1 HV3I_HUMAN	P01770 homo sapien
6	407.5	60.9	122	1 HV3H_HUMAN	P01769 homo sapien
7	403.5	60.3	119	1 HV38_MOUSE	P01768 mus musculu
8	401	59.9	115	1 HV3D_HUMAN	P01776 homo sapien
9	400.5	59.9	117	1 HV30_HUMAN	P01776 homo sapien
10	400.5	59.9	122	1 HV20_MOUSE	P01769 mus musculu
11	400	59.8	123	1 HV23_MOUSE	P01782 mus musculu
12	399.5	59.7	116	1 HV3T_HUMAN	P01781 homo sapien
13	399	59.6	117	1 HV3C_HUMAN	P01765 homo sapien
14	399	59.6	123	1 HV22_MOUSE	P01791 mus musculu
15	398.5	59.6	114	1 HV3B_HUMAN	P01763 homo sapien
16	398	59.5	123	1 HV25_MOUSE	P01794 mus musculu
17	396.5	59.3	122	1 HV21_MOUSE	P01780 mus musculu
18	396	59.2	119	1 HV3L_HUMAN	P01773 homo sapien
19	395.5	59.1	122	1 HV3A_HUMAN	P01773 homo sapien
20	394	58.9	123	1 HV18_MOUSE	P01787 mus musculu
21	393	58.7	120	1 HV3E_HUMAN	P01766 homo sapien
22	393	58.7	123	1 HV19_MOUSE	P01788 mus musculu
23	389	58.1	115	1 HV3F_HUMAN	P01767 homo sapien
24	388	58.0	123	1 HV24_MOUSE	P01793 mus musculu
25	388	58.0	144	1 HV26_MOUSE	P01795 mus musculu
26	387.5	57.9	119	1 HV3N_HUMAN	P01775 homo sapien
27	387	57.8	117	1 HV02_CANPA	P01785 canis fami
28	384.5	57.5	114	1 HV01_CANPA	P01784 canis fami
29	382.5	57.2	119	1 HV37_MOUSE	P01807 mus musculu
30	380	56.8	115	1 HV32_MOUSE	P01801 mus musculu
31	379.5	56.7	119	1 HV3M_HUMAN	P01774 homo sapien
32	378	56.5	113	1 HV30_MOUSE	P01739 mus musculu
33	375.5	56.1	111	1 HV35_MOUSE	P01804 mus musculu

34	375.5	56.1	119	1 HV40_MOUSE	P01810 mus musculu
35	373.5	55.8	120	1 HV3J_HUMAN	P01782 homo sapien
36	373	55.8	113	1 HV2J_MOUSE	P01796 mus musculu
37	371.5	55.5	116	1 HV05_CARAU	P01811 carassius a
38	371	55.5	142	1 HV01_RAT	P01805 rattus norv
39	370	55.3	117	1 HV17_MOUSE	P01786 mus musculu
40	369	55.2	115	1 HV33_MOUSE	P01802 mus musculu
41	368	55.0	113	1 HV31_MOUSE	P01800 mus musculu
42	368	55.0	118	1 HV28_MOUSE	P01809 mus musculu
43	367	54.9	113	1 HV28_MOUSE	P01797 mus musculu
44	366	54.7	117	1 HV41_MOUSE	P01811 mus musculu
45	364.5	54.5	119	1 HV3P_HUMAN	P01777 homo sapien

ALIGNMENTS

RESULT 1

ID	HV3J_HUMAN	STANDARD;	PRT;	121 AA.
AC	P01771;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig heavy chain V-II1 region H1L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=79124695; PubMed=420800;			
RT	Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;			
RT	"Amino acid sequence of the VH region of human myeloma			
RT	cryoglobulin IgG H1L."			
RL	Biochemistry 18:553-560 (1979).			
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA			
CC	PROTEIN.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR; A02054; GIHHD.			
DR	HSSP; P01772; 2PB4.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	SMART; SM00406; IGV; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region; Pyroliidone carboxylic acid.			
FT	DOMAIN 1 112			
FT	MOD RES 1 1			
FT	NON TER 121 121			
SO	SEQUENCE 121 AA; 13566 MW; 480FC53610BF5DAB CRC64;			

Query Match 70.3%; Score 470; DB 1; Length 121;
Best Local Similarity 68.0%; Pred. No. 1.8e-41;
Matches 85; Conservative 20; Mismatches 16; Indels 4; Gaps 2;

QY	1 QVTLSSGGVVGPGSLRVACVAGFTFNNPQMWVRQAPGKLEWAFIWDASNGKY 60	
DB	1 QVTLVQAGGVVPGGSLRVACVAGFTFNNPQMWVRQAPGKLEWAFIWDASNGKY 60	
QY	61 GDSVGRFTFSRDNSTKTYLQNNGLRAEDTAVYCCAREKAVRGISRYNYMDVGKGT 120	
DB	61 GDSVGRFTFSRDNSTKTYLQNNGLRAEDTAVYCCAREKAVRGISRYNYMDVGKGT 120	
QY	121 VYVSS 125	
DB	117 VYVSS 121	

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RESULT 2
RT HV3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region CAM.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=81013859; PubMed=6774332;
RX Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC -1- SIMILARITY: Contains 1 Immunoglobulin-like domain.
CC PIR; A02051; M3HUM.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrolydome carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
FT SEQUENCE 122 AA; 13668 MW; A42DPF17D25F1C2 CRC64;
SQ
Query Match 68.8%; Score 460.5; DB 1; Length 122;
Best Local Similarity 67.5%; Pred. No. 1,7e-40;
Matches 85; Conservative 19; Mismatches 17; Indels 5; Gaps 2;
QY 1 QVTLSEGSGGVNPGGSLRVAACVAGFTFRFGHMYRQAPGKGLWVAIFPDASNKGY 60
DB 1 QVTLSEGSGGVNPGGSLRVAACVAGFTFRFGHMYRQAPGKGLWVAIFPDASNKGY 60
QY 61 GDSVKGFTVSRDNRKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIR-YNYNDVWGKGT 119
DB 61 GDSVKGFTVSRDNRKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIR-YNYNDVWGKGT 119
QY 61 ABSVKGFTISRDRSKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIR-YNYNDVWGKGT 116
DB 61 ABSVKGFTISRDRSKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIR-YNYNDVWGKGT 116
QY 120 VTWVS 125
DB 120 VTWVS 125
QY 117 LTVSS 122
DB 117 LTVSS 122

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RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637 (1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=7100368; PubMed=401950;
RA Adegusbo K., Milestein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304 (1977).
CC -----
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CC -----
CC EMBL; J00522; AAD15290.1; -
CC PIR; E90809; GIMS21.
CC PDB; 1IGC; 03-JUN-95.
CC InterPro; IPR007110; Ig_Like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; IGV; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON_TER 1 1
FT SIGNAL 1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 115 115 DN -> H (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT NON_TER 136 136 Y -> W (IN REF. 2).
FT SEQUENCE 136 AA; 15071 MW; 2276A9BDBDF016 CRC64;
SQ
Query Match 64.8%; Score 433.5; DB 1; Length 136;
Best Local Similarity 66.4%; Pred. No. 1.1e-37;
Matches 83; Conservative 16; Mismatches 19; Indels 7; Gaps 2;
QY 2 VKTLSEGSGGVNPGGSLRVAACVAGFTFRFGHMYRQAPGKGLWVAIFPDASNKGY 61
DB 18 VQTLSEGSGGVNPGGSLRVAACVAGFTFRFGHMYRQAPGKGLWVAIFPDASNKGY 77
QY 62 DSVKGRFTVSRDNRKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIRYNY-MDVWGKGT 120
DB 62 DSVKGRFTVSRDNRKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIRYNY-MDVWGKGT 120
QY 78 DTVKGRFTISRDRSKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIRYNY-MDVWGKGT 131
DB 78 DTVKGRFTISRDRSKNTLYLQNNGLRAEDTAVYVCAREKAVRGISIRYNY-MDVWGKGT 131
QY 121 VTWVS 125
DB 121 VTWVS 125
QY 132 VTWVS 136
DB 132 VTWVS 136

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RESULT 3
ID HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paekind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

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RESULT 4
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
ID HV3K_HUMAN
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region KOL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=813289131; PubMed=6884994;

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RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Margaret M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
 and 1.0 A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02055; G1HUKL.

DR PDB; 2FB4; 12-JUL-89.
 DR PDB; 2IC3; 12-JUL-89.

DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.

KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96

FT STRAND 105 110
 FT STRAND 3 7

FT STRAND 11 12
 FT TURN 14 15

FT STRAND 18 25
 FT HELIX 29 31

FT STRAND 34 39
 FT TURN 41 42

FT STRAND 45 51
 FT TURN 53 54

FT STRAND 58 60
 FT HELIX 62 64

FT STRAND 65 65
 FT TURN 66 67

FT STRAND 68 73
 FT TURN 74 77

FT STRAND 78 83
 FT HELIX 88 90

FT STRAND 92 99
 FT STRAND 106 106

FT TURN 107 108
 FT STRAND 109 109

FT STRAND 113 116
 FT STRAND 120 124

FT NON_TER 126 126
 SO SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 64.1%; Score 428.5; DB 1; Length 126;
 Best Local Similarity 65.1%; Pred. No. 3,4e-37;
 Matches 82; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

QY 1 QVLTLESGGVVOPGSLRACVAGSFTFRNFGMHVWROAPGKLEWVAFIMFDASNGY 60
 Db 1 QVLTLESGGVVOPGSLRACVAGSFTFRNFGMHVWROAPGKLEWVAFIMFDASNGY 60

QY 61 GDSVKGKFTVSRDINSKNTLYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 119
 Db 61 ADSVKGKFTVSRDINSKNTLYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 119

QY 120 TVTVSS 125
 Db 121 TVTVSS 126

QY 120 TVTVSS 125
 Db 121 TVTVSS 126

RESULT 5
 ID HV31_HUMAN STANDARD; PRT; 119 AA.
 AC P01770;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region NIE.

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

OX [1]
 RN SEQUENCE.

RX MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;

RT "The rule of antibody structure. The primary structure of a
 monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
 chymotryptic peptides of the H-chain, alignment of the tryptic
 peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

CC CC
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96

FT STRAND 119 119
 FT NON_TER 119 119

SO SEQUENCE 119 AA; 13242 MW; C96935A6B55E165B CRC64;

Query Match 62.3%; Score 417; DB 1; Length 119;
 Best Local Similarity 63.2%; Pred. No. 4.8e-36;
 Matches 79; Conservative 19; Mismatches 21; Indels 6; Gaps 2;

QY 1 QVLTLESGGVVOPGSLRACVAGSFTFRNFGMHVWROAPGKLEWVAFIMFDASNGY 60
 Db 1 QVLTLESGGVVOPGSLRACVAGSFTFRNFGMHVWROAPGKLEWVAFIMFDASNGY 60

QY 61 GDSVKGKFTVSRDINSKNTLYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 120
 Db 61 ADSVKGKFTVSRDINSKNTLYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 120

QY 121 TVTVSS 125
 Db 121 TVTVSS 119

QY 121 TVTVSS 125
 Db 121 TVTVSS 119

QY 121 TVTVSS 125
 Db 121 TVTVSS 119

QY 121 TVTVSS 125
 Db 121 TVTVSS 119

QY 121 TVTVSS 125
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QY 121 TVTVSS 125
 Db 121 TVTVSS 119

QY 121 TVTVSS 125
 Db 121 TVTVSS 119

QY 121 TVTVSS 125
 Db 121 TVTVSS 119

QY 121 TVTVSS 125
 Db 121 TVTVSS 119

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DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE Ig heavy chain V-II region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human Igm immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02052; M3HUGA.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 112 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 1 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match
Best Local Similarity 56.6%; Score 407.5; DB 1; Length 122;
Matches 73; Conservative 25; Mismatches 20; Indels 11; Gaps 2;

QY 1 QVLTLESGGGVQPGSLRVACVAGFTFRNFGMHVWRQAPGKGLWVAFIMPDASNKGY 60
DB 1 QVLTLESGGGVQPGSLRVACVAGFTFRNFGMHVWRQAPGKGLWVAFIMPDASNKGY 60
QY 61 GDSVKGKFTVSRNSKNTLYLQWNGLRAPETAVYYCARE---KAVRGISRYNYMDVWGCTT 116
DB 61 GDSVKGKFTVSRNSKNTLYLQWNGLRAPETAVYYCARE---KAVRGISRYNYMDVWGCTT 116
QY 61 AASVKGKFTVSRNSKNTLYLQWNGLRAPETAVYYCARE---KAVRGISRYNYMDVWGCTT 116
DB 61 AASVKGKFTVSRNSKNTLYLQWNGLRAPETAVYYCARE---KAVRGISRYNYMDVWGCTT 116
QY 117 KGTIVTVSS 125
DB 114 ZGTLVTVSS 122

RESULT 7
HV38 MOUSE STANDARD; PRT; 119 AA.
AC P01808;
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE Ig heavy chain V region T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerogonathi; Muridae; Murinae; Mus.
ON NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudnikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.

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CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02078; AWM5T6.
DR HSSP; P01810; 2PB4.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6FA00E8 CRC64;

Query Match
Best Local Similarity 62.4%; Score 403.5; DB 1; Length 119;
Matches 78; Conservative 18; Mismatches 22; Indels 7; Gaps 2;

QY 1 QVLTLESGGGVQPGSLRVACVAGFTFRNFGMHVWRQAPGKGLWVAFIMPDASNKGY 60
DB 1 EVLTLESGGGVQPGSLRVACVAGFTFRNFGMHVWRQAPGKGLWVAFIMPDASNKGY 60
QY 61 GDSVKGKFTVSRNSKNTLYLQWNGLRAPETAVYYCAREKAVRGISRYNYMDVWGCTT 120
DB 61 GDSVKGKFTVSRNSKNTLYLQWNGLRAPETAVYYCAREKAVRGISRYNYMDVWGCTT 120
QY 121 VTVSS 125
DB 114 VTVSS 118

RESULT 8
HV3D HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE Ig heavy chain V-II region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGC2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02048; H3HUTL.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 108
FT NON_TER 1 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match
Best Local Similarity 59.9%; Score 401; DB 1; Length 115;
Matches 62.4%; Pred. No. 2.1e-34;

```


	Matches	78;	Conservative	16;	Mismatches	21;	Indels	10;	Gaps	2.
QY	1	QVKLLSEGGGVVOPGSGLRVACVNSGLFFFRKFNFGHHVRQAEPCKGLEWVAFTWFDSANKGY	60							
Dd	1	EVOLLSEGGGVVOPGSGLRRLSCASGLFFPSTVMSVMWAQAPCKGLZMGALIZGLSVSSZSY	60	:	:	:	:	:	:	:
QY	61	GDSVKGRTVASRDNRSKNLFLYQMNGLRADPTAVVVYCAREKAVRGISRNNYYIMDWGSKCTT	120	:	:	:	:	:	:	:
Dd	61	ABSVKGRITTSIRDSKNT---MSLRPEDTAIVVYCAKGVSA-----YYFBYGZDTTL	110	:	:	:	:	:	:	:
QY	121	VTVVS	125	:	:	:	:	:	:	:
Dd	111	VTVSS	115	:	:	:	:	:	:	:

ID	HY30_HUMAN	STANDARD;	PRT;	117 AA.
AC	P01776;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig heavy chain V-II region WMS.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
CC	NCBI_TaxID=9606;			
CC	[1]			
CC	SEQUENCE			
CC	MEDLINE=74142702; PubMed=4522793;			
CC	Capra U.D., Kenoe J.M.;			
CC	"Variable region sequences of five human immunoglobulin heavy chains			
CC	of the VH3 subgroup: definitive identification of four heavy chain			
CC	hypervariable regions.";			
CC	Proc. Natl. Acad. Sci. U S A. 71:845-848 (1974).			
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA			
CC	PROTEIN.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
CC	PIR; A02059; GIHW5.			
CC	HSSP; P01772; 2PB4.			
CC	GO; GO:0005576; C:extracellular; NAS.			
CC	GO; GO:0003823; P:antigen binding activity; NAS.			
CC	GO; GO:0069555; P:immune response; NAS.			
CC	InterPro; IPR007110; IG-1like.			
CC	InterPro; IPR003006; IG_MHC.			
CC	InterPro; IPR003596; IG_V.			
CC	Pfam; PF00047; I97.1.			
CC	SMART; SM00406; IGV; 1.			
CC	PROSITE; PS50835; IG_LIKE; 1.			
CC	Immunoglobulin V region.			
CC	DOMAIN 1 112 IG-LIKE.			
CC	NON TER 117 117			
CC	SEQUENCE 117 AA; 13091 MW; 201DEF0E1E53D9BF CRC64;			
CC	Query Match 59.9%; Score 400.5; DB 1; Length 117;			
CC	Best Local Similarity 61.5%; Pred. No. 2,4e-34;			
CC	Matches 75; Conservative 22; Mismatches 20; Indels 5; Gaps			
CC	QY 1 OKLLESGGGVVPQGGSLRVACVAGSPFFNFGMHWROAPRGLEWNAFTIFPDSNKGK			
CC	DB 1 EYQLLESGGGVLPQGGSLRVACVAGSPFFNFGMHWROAPRGLEWNAFTIFPDSNKGK			
CC	QY 61 GPSVKGRFVSNDSKNLTLYLQNNGLRAEDPTAVYYCARERAVAGISRVNYVMYDVGKGGT			
CC	DB 61 ADTVNGRFTISNDSKNLTLYLQNNGLRAEDPTAVYYCARERAVAGISRVNYVMYDVGKGGT			
CC	QY 121 VT 122			
CC	DB 116 VT 117			

AC	HW20 MOUSE	STANDARD;	PRT;	122 AA.
AD	P01789;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	IG heavy chain V region M603.			
OS	Mus musculus (Mouse).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=60199926; PubMed=6769593;			
RA	Early P., Huang H., Davis M., Calame K., Hood L.;			
RT	"An immunoglobulin heavy chain variable region gene is generated from			
RT	three segments of DNA: VH, D and JH.";			
RL	Cell 19:981-992(1980).			
RN	[2]			
RP	SEQUENCE OF 1-120.			
RX	MEDLINE=75017346; PubMed=4213577;			
RA	Rudikoff S., Potter M.;			
RT	"Variable region sequence of the heavy chain from a phosphorylcholine			
RT	binding myeloma protein.";			
RL	Biochemistry 13:4033-4038(1974).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.			
RX	MEDLINE=75065510; PubMed=4530984;			
RA	Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,			
RA	Davis D.R.;			
RT	"The three-dimensional structure of a phosphorylcholine-binding mouse			
RT	immunoglobulin Fab and the nature of the antigen binding site.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).			
CC	1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT			
CC	BINDS PHOSPHORYLCHOLINE.			
CC	1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PDB; B90795; ATMS63.			
DR	PDB; 1MCP; 15-JUL-92.			
DR	PDB; 2MCP; 15-JUL-92.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG_1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin V region; 3D-structure.			
FT	SITE	1	121	IG-LIKE.
FT	SITE	33	33	H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
FT	SITE	52	52	PHORYLCHOLINE.
FT	SITE	52	52	H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
FT	SITE	52	52	PHORYLCHOLINE.
FT	STRAND	3	7	
FT	STRAND	11	12	
FT	TURN	14	15	
FT	TURN	17	25	
FT	STRAND	30	31	
FT	TURN	33	39	
FT	STRAND	41	42	
FT	TURN	46	50	
FT	STRAND	54	55	
FT	TURN	61	61	
FT	STRAND	64	69	
FT	TURN	70	75	
FT	STRAND	76	79	
FT	TURN	80	86	
FT	STRAND	90	92	
FT	HELEX	94	103	
FT	STRAND	107	112	
FT	STRAND	116	120	
FT	NON TER	122	122	
SQ	SEQUENCE	122 AA;	13626 MW;	BA2C864438B64F0F CRC64;
Query Match		59.9%;	Score 400.5;	DB 1; Length 122;
Best Local Similarity		61.0%;	Pred. No. 2.5e-34;	

RESULT 10
HV20_MOUSE

Query Match	59.9%	Score 400.5;	DB 1;	Length 122;
Best Local Similarity	61.0%;	Pred. NO. 2.5e-34;		

Matches 83; Conservative 11; Mismatches 17; Indels 25; Gaps 4;

QY 1 QVLLSEGGGVNPGGSLRVAACVAGSGTFPRNFGHMWROAPGKLEWAFIWPASNGK- 59
 Db 1 EVKLVEGGGGLVPGGSLRLSCATSGTFPSDFYEMWROPGKLEWIA-----ASRNKGN 56
 60 -----YGDVSKGRFTVSRNSKNTLYLQWNGLRADTAAYVYCAEKAVERGISRYNY---- 110
 QY 57 KYTTEYASVSKGRFTVSRDTSQSLTYLQWNLRAEDTAIYCA-----NYGST 106
 Db 111 -YMDVWKGTTVTYSS 125
 107 WYFDVWAGTTVTYSS 122

RESULT 11
 HV33_MOUSE STANDARD; PRT; 123 AA.
 AC P01792;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region HPCG8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=8197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than
 RT their IGM counterparts";
 RL Nature 251:23-34(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS PHOSPHORYLCHOLINE.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Hybridoma.
 KW DOMAIN 1 114 IG-LIKE.
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAFE7D8D CRC64;

Query Match 59.8%; Score 400; DB 1; Length 123;
 Best Local Similarity 64.1%; Pred. No. 2.8e-34;
 Matches 84; Conservative 13; Mismatches 20; Indels 14; Gaps 5;

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region GAL.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=75059123; PubMed=4803843;
 RA Metanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IGM-immunoglobulin
 RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 RT type), subgroup H III. Architecture of the complete IGM-molecule";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN (2)
 RP REVISION TO 28-33.
 RA Hilschmann N.;
 RL Submitted (JUN-1975) to the FIR data bank.
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 112 IG-LIKE.
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 59.7%; Score 399.5; DB 1; Length 116;
 Best Local Similarity 63.2%; Pred. No. 3e-34;
 Matches 79; Conservative 16; Mismatches 21; Indels 9; Gaps 2;

QY 1 QVLLSEGGGVNPGGSLRVAACVAGSGTFPRNFGHMWROAPGKLEWAFIWPASNGK- 60
 Db 1 EVKLVEGGGGLVPGGSLRLSCATSGTFPSDFYEMWROPGKLEWIA-----ASRNKGN 56
 61 -----YGDVSKGRFTVSRNSKNTLYLQWNGLRADTAAYVYCAEKAVERGISRYNYMDV 114
 QY 57 KYTTEYASVSKGRFTVSRDTSQSLTYLQWNLRAEDTAIYCA-----NYGST 106
 Db 111 -YMDVWKGTTVTYSS 125
 107 WYFDVWAGTTVTYSS 122

RESULT 13
 HV33_MOUSE STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region VH26 precursor.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8101090; PubMed=6450418;
 RA Macthysens G., Rabbits T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 RT heavy chain variable region";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@ebi.ebi.ch).
CC
DR EMBL: J00236; AAA5516.1; -
DR EMBL: M35415; AAA58735.1; -
DR PIR: A02047; H3H26.
DR PDB: 1H0J; 23-DEC-99.
DR Genew: HGNC:5545; IGHV.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
KW SIGNAL 1 19 IG HEAVY CHAIN V-III REGION VH26.
FT CHAIN 20 117
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
Query Match 59.6%; Score 399; DB 1; Length 117;
Best Local Similarity 75.5%; Pred. No. 3.4e-34;
Matches 74; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
QY 1 QVLTLESGGGLVPGGSLRACVAGFTFRNFGMHVWRQAPGKGLFWAFIFDASNKGY 60
DB 20 EVQLLESGGGLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVAISGSGSTYY 79
QY 61 GDSVKGRTVSRNDSKNTLYLQMGRLAEDTAVYYCAK 98
DB 80 GDSVKGRTVSRNDSKNTLYLQMGSLRAEDTAVYYCAK 117
RESULT 14
HV22_MOUSE STANDARD; PRT; 123 AA.
AC P01791;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region HPCMO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=8197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 114 IG-LIKE.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;
Query Match 59.6%; Score 399; DB 1; Length 123;
Best Local Similarity 61.2%; Pred. No. 3.5e-34;
Matches 82; Conservative 13; Mismatches 19; Indels 20; Gaps 4;
QY 1 QVLTLESGGGLVPGGSLRACVAGFTFRNFGMHVWRQAPGKGLFWAFIFDASNKGY 59
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSDFMEWVRQPPGKRLRWIA-----ASHKKN 56
QY 60 -----YGDVKGRTVSRNDSKNTLYLQMGRLAEDTAVYYCAKREAVAGISRYN---Y 111
DB 57 DYTTESASVKGRTVSRNDSKNTLYLQMGRLAEDTAVYYCAKREAVAGISRYN---Y 109
QY 112 MDVWKGRTVTVSS 125
DB 110 FDVWKGRTVTVSS 123
RESULT 15
HV23_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P01772; 2F84.
DR PIR: A02046; M3HWE.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;
Query Match 59.6%; Score 398.5; DB 1; Length 114;
Best Local Similarity 62.4%; Pred. No. 3.7e-34;
Matches 78; Conservative 18; Mismatches 18; Indels 11; Gaps 1;
QY 1 QVLTLESGGGLVPGGSLRACVAGFTFRNFGMHVWRQAPGKGLFWAFIFDASNKGY 60
DB 1 QVQLVDSGGGLVPGGSLRLSCAASGFTFSANDMWRQAPGKGLEWISFISGSGSTYY 60
QY 61 GDSVKGRTVSRNDSKNTLYLQMGRLAEDTAVYYCAKREAVAGISRYNVDVWKGRTT 120

Db 61 AD5VKGRFTISRNBKNSLYLQWSSLRAEDTAVYYCARG-----MLNMGQTL 109

QY 121 VTVSS 125

Db 110 VTVSS 114

Search completed: January 22, 2004, 11:51:48
Job time : 10.8696 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	483	72.2	113	4	Q9U190	Q9u190 homo sapien
2	480.5	71.8	613	4	Q8WUK1	Q8wuk1 homo sapien
3	457	68.3	499	4	Q8NSK4	Q8nsk4 homo sapien
4	456.5	68.2	573	4	Q8WU38	Q8wu38 homo sapien
5	449	67.1	121	4	Q9U171	Q9u171 homo sapien
6	448.5	67.0	132	4	Q9U184	Q9u184 homo sapien
7	446	66.7	116	4	Q9U193	Q9u193 homo sapien
8	443	66.2	493	4	Q8NCL6	Q8ncl6 homo sapien
9	441.5	66.0	471	4	Q8CT77	Q8ct77 homo sapien
10	435.5	65.1	112	4	Q9HC11	Q9hc11 homo sapien
11	433.5	64.8	147	4	Q9Y509	Q9y509 homo sapien
12	431	63.5	597	4	Q96BB9	Q96bb9 homo sapien
13	424.5	63.4	473	11	Q91Z05	Q91z05 mus muscul
14	423.5	63.3	118	4	Q9U191	Q9u191 homo sapien
15	401.5	60.0	118	4	Q9U172	Q9u172 homo sapien
16	398.5	59.6	494	4	Q96K68	Q96k68 homo sapien

17	394	58.9	479	11	Q91WP5	Q91WP5 mus musculus
18	393.5	58.8	487	11	Q99XZ4	Q99XZ4 mus musculus
19	385.5	57.6	469	11	Q8R3V9	Q8R3V9 mus musculus
20	384.5	57.5	484	11	Q8VEA0	Q8VEA0 mus musculus
21	383	57.2	95	4	Q9ULB6	Q9ULB6 homo sapien
22	383	57.2	119	11	Q92OE7	Q92OE7 mus musculus
23	380	56.8	480	11	Q91XE1	Q91XE1 mus musculus
24	378	56.5	486	11	Q91Z07	Q91Z07 mus musculus
25	376	56.2	521	4	Q8NA49	Q8NA49 homo sapien
26	370.5	55.4	298	11	Q9OYF0	Q9OYF0 mus musculus
27	367	54.9	104	4	Q9UL87	Q9UL87 homo sapien
28	361	54.0	131	4	Q9UL88	Q9UL88 homo sapien
29	351.5	52.5	124	6	Q9N0W6	Q9N0W6 homo sapien
30	350.5	52.4	124	6	Q9N0M4	Q9N0M4 oryctolagus
31	342.5	51.2	159	4	Q9G0S0	Q9G0S0 homo sapien
32	338.5	50.6	500	4	Q9BRX0	Q9BRX0 homo sapien
33	335	50.1	125	4	Q9UL95	Q9UL95 homo sapien
34	334.5	50.0	124	4	Q9UL92	Q9UL92 homo sapien
35	334.5	50.0	437	11	Q9R1A4	Q9R1A4 mus musculus
36	332	49.6	112	4	Q9UGJ3	Q9UGJ3 homo sapien
37	331.5	49.6	241	11	Q921A6	Q921A6 mus musculus
38	329.5	49.3	121	11	Q99NG4	Q99NG4 mus musculus
39	327	48.9	484	11	Q991A6	Q991A6 mus musculus
40	317.5	47.5	145	11	Q92XR3	Q92XR3 mus musculus
41	316	47.2	119	4	Q9UL94	Q9UL94 homo sapien
42	313.5	46.9	482	11	Q91X92	Q91X92 mus musculus
43	312.5	46.7	613	11	Q8VCX7	Q8VCX7 mus musculus
44	311	46.5	119	5	Q9GVZ2	Q9GVZ2 schistosoma
45	309	46.2	117	11	Q9QXF0	Q9QXF0 mus musculus

ALIGNMENTS

RESULT 1

ID	Q9UL90	PRELIMINARY;	PRT;	113	AA
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DT	01-MAY-2000	(TREMBlrel. 13, Created)
DT	01-MAY-2000	(TREMBlrel. 13, Last sec

01-MAR-2003 (ITEMBLER. 23, last annotation update)

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DE      (Eragmenc) :
OS      Homo sapiens (Human) :
```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RX MEDLINE=98277139; PubMed=9614934;

Young D.C.;

RI lectus.,"
clin. Immunol. 87:184-192(1998).

DR HSSP: P01772; 2FB4.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

SO	113	AA:	12437	MM:
FF	113			
NON	TER			
SEQUENCE				

Query Match 72.28:

Matches 90; Conservative 14

QY 1 QVKLESGGGVQPGGSLRV

```
Db      1 EVOLVESGGGVPGGSLRLSCAASGFTFSYGVHWRQAPGKGLWVAFIKYDGSNKYY 60
Qy      61 GDSYKGRFTVSRDMSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
Db      61 ADSYKGRFTISRDNKNTLYLQNMGLRAEDTAVYYCAKD-----LNYWGQGT 108
Qy      121 VTWSS 125
Db      109 VTWSS 113

RESULT 2
Q8WUK1  PRELIMINARY; PRT; 613 AA.
AC      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS      Hypothetical protein.
OC      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RA      Strauberg R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC020240; AAH20240.1; -.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; IG_5.
DR      SMART; SM00406; IGv_1.
DR      PROSITE; PS50835; IG_LIKE; 5.
DR      PROSITE; PS00290; IG_MHC; 3.
KW      Hypothetical protein.
SQ      SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match
Best Local Similarity 71.8%; Score 480.5; DB 4; Length 613;
Matches 91; Conservative 15; Mismatches 14; Indels 5; Gaps 2;

Qy      1 QVLLSEGGGVVPGGSLRVACVAGFTFRNFGMHWRQAPGKGLWVAFIWPDASNKGY 60
Db      20 QVQLVESGGGVVQPGSLRLSCAASGFTFSYGVHWRQAPGKGLWVAIVSYGSNKYY 79
Qy      61 GDSYKGRFTVSRDMSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
Db      80 ADSYKGRFTISRDNKNTLYLQNMGLRAEDTAVYYCAWDWS-EGVETP---DIMGQGT 134
Qy      121 VTWSS 125
Db      135 VTWSS 139

RESULT 3
Q8NSK4  PRELIMINARY; PRT; 499 AA.
AC      01-OCT-2002 (TREMBLrel. 22, Created)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS      Hypothetical protein.
OC      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Blood;
RA      Strauberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
```

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DR      EMBL; BC032249; AAH32249.1; -.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG_CL.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; IG_4.
DR      SMART; SM00409; IG; 4.
DR      SMART; SM00407; IGG1; 2.
DR      SMART; SM00406; IGv_1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match
Best Local Similarity 68.3%; Score 457; DB 4; Length 499;
Matches 87; Conservative 16; Mismatches 22; Indels 2; Gaps 1;

Qy      1 QVLLSEGGGVVPGGSLRVACVAGFTFRNFGMHWRQAPGKGLWVAFIWPDASNKGY 60
Db      20 EVOLVESGGGVVPGGSLRLSCAASGFTFPDSSGASVWRQAPGKGLWVSIINNGSTNY 79
Qy      61 GDSYKGRFTVSRDMSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGK 118
Db      80 ADSYKGRFTISRDNKNTLYLQNMGLRAEDTAVYYCAKSGSGSCLGYTMDVWGK 139
Qy      119 TTYTVSS 125
Db      140 TTYTVSS 146

RESULT 4
Q8WU38  PRELIMINARY; PRT; 573 AA.
AC      Q8WU38;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Hypothetical protein.
OC      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RA      Strauberg R.;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC021276; AAH21276.1; -.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; IG; 4.
DR      SMART; SM00406; IGv_1.
DR      PROSITE; PS50835; IG_LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match
Best Local Similarity 68.2%; Score 456.5; DB 4; Length 573;
Matches 86; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

Qy      1 QVLLSEGGGVVPGGSLRVACVAGFTFRNFGMHWRQAPGKGLWVAFIWPDASNKGY 60
Db      20 EVOLVESGGGVVPGGSLRLSCAASGFTFPDYAMHWRQAPGKGLWVSGISWNSGSIY 79
Qy      61 GDSYKGRFTVSRDMSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
Db      80 ADSYKGRFTISRDNKNTLYLQNMGLRAEDTAVYYCAKSGSGSITG-YTGMVWGQGT 138
Qy      121 VTWSS 125
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Db 61 DSVKGRFTIRSDNSKNTLYLQWNGSLRAEDTAVYYCA---GGGGG-----LGWVGQSTLV 112
QY 122 TVSS 125
Db 113 TVSS 116

RESULT 8
Q8NCL6 PRELIMINARY; PRT; 493 AA.
AC Q8NCL6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein FLJ90170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Isegai T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074651; BAC1114.1; -.
DR InterPro; IPR003599; IG_1ike.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00407; IG_4.
DR SMART; SM00409; IGL_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;

Query Match 66.2%; Score 443; DB 4; Length 493;
Best Local Similarity 67.2%; Pred. No. 2.6e-36;
Matches 84; Conservative 16; Mismatches 21; Indels 4; Gaps 2;
```

```
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF58660E CRC64;

Query Match 66.0%; Score 441.5; DB 4; Length 471;
Best Local Similarity 66.4%; Pred. No. 3.5e-38;
Matches 83; Conservative 23; Mismatches 16; Indels 3; Gaps 2;
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```
QY 1 QVLTLSGGGVNPGSLRACVAGSFTFRNFGMHWRQAPGKLEWVAFIWFDAVNKG 60
Db 20 EVQLVESGGGLVPRGSLRSCAASGFTFSYSMHWROAPGKLEWVSMSSSTIYY 79
QY 61 GDSVKGRTFVSRRNSKNTLYLQWNGSLRAEDTAVYYCAREKAVRGISRYNYMDVGKGT 120
Db 80 ADSVKGRTFVSRRNSKNTLYLQWNGSLRAEDTAVYYCARD--LQQLTNSY-WYFDLWGKGL 136
QY 121 TVSS 125
Db 137 TVSS 141

RESULT 10
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Single Chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Teujimoto Y., Aada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: isolation from a
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSP; P01772; 2F84.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match 65.1%; Score 435.5; DB 4; Length 112;
Best Local Similarity 66.1%; Pred. No. 2.5e-38;
Matches 80; Conservative 18; Mismatches 14; Indels 9; Gaps 1;
```


Db 61 ADGVKGRFTISRDNKNTLYLQNMNSLRADPTAVYCAKRR-----YALDYMGGTL 111
 QY 121 V 121
 Db 112 V 112

RESULT 11

Q9Y509 PRELIMINARY; PRT; 147 AA.

AC Q9Y509; PRELIMINARY; PRT; 147 AA.
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE V33 protein (Fragment).
 GN V33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_Taxid=9606;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=96071149; PubMed=7475288;
 RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
 RA Lichtenstein A.R., Berenson J.R.;
 RT "A CD10-positive subset of malignant cells is identified in multiple
 RT myeloma using PCR with patient-specific immunoglobulin gene primers."
 RL Leukemia 9:1948-1953(1995).
 DR EMBL; S80860; AAD14339.1; -.
 DR HSSP; P01772; 2FB4.
 DR InterPro: IPR007110; IG_Like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG_Like; 1.
 DR NON TER
 FT 1
 SQ SEQUENCE 147 AA; 15768 MW; 8489FCMAA7BC925C CRC64;

Query Match 64.8%; Score 433.5; DB 4; Length 147;
 Best Local Similarity 66.1%; Pred. No. 5.8e-38;
 Matches 84; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

QY 1 QVTLSSGGGVOPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIFDASNKGY 60
 Db 1 QVHLVSSGGGVOPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIFDASNKGY 60
 QY 61 GDSVKGRTVSRDNRKNTLYLQNMNSLRADPTAVYCAKRR-KAVRGISRYNYMDVMGKGT 119
 Db 61 AGSVKGRFTISRDNKNTLYLQNMNSLRADPTAVYCAKRR-KAVRGISRYNYMDVMGKGT 120
 QY 120 TVTVSS 125
 Db 121 LVTYSS 126

RESULT 12

Q96BB9 PRELIMINARY; PRT; 597 AA.

AC Q96BB9; PRELIMINARY; PRT; 597 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_Taxid=9606;
 RX SEQUENCE FROM N.A.
 RA TISSUE=B-cell;
 RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC015760; AA115760.1; -.
 DR InterPro: IPR007110; IG_Like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG_Like; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E6CE263D9 CRC64;

Query Match 64.4%; Score 431; DB 4; Length 597;
 Best Local Similarity 66.1%; Pred. No. 6.1e-37;
 Matches 84; Conservative 17; Mismatches 22; Indels 4; Gaps 2;

QY 1 QVTLSSGGGVOPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIFDASNKGY 60
 Db 20 EVQLVSSGGGVOPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIFDASNKGY 79
 QY 61 GDSVKGRTVSRDNRKNTLYLQNMNSLRADPTAVYCAKRR-KAVRGISRYNYMDVMGKGT 118
 Db 80 ADGVKGRFTISRDNKNTLYLQNMNSLRADPTAVYCAKRR-KAVRGISRYNYMDVMGKGT 137
 QY 119 TVTVSS 125
 Db 138 LVTYSS 144

RESULT 13

Q91205 PRELIMINARY; PRT; 473 AA.

AC Q91205; PRELIMINARY; PRT; 473 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 51.9 kDa protein.
 GN A0044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RX SEQUENCE FROM N.A.
 RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010327; AA110327.1; -.
 DR MGI; MGI:2144967; A0044919.
 DR InterPro: IPR000345; CytC_heme_bind.
 DR InterPro: IPR007110; IG_Like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS00190; CYTOCHROME C; 1.
 DR PROSITE; PS50835; IG_Like; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.5%; Score 424.5; DB 11; Length 473;
 Best Local Similarity 63.2%; Pred. No. 2.2e-36;
 Matches 79; Conservative 22; Mismatches 17; Indels 7; Gaps 1;

QY 1 QVTLSSGGGVOPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIFDASNKGY 60
 Db 20 EVQLVSSGGGVOPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIFDASNKGY 79
 QY 61 GDSVKGRTVSRDNRKNTLYLQNMNSLRADPTAVYCAKRR-KAVRGISRYNYMDVMGKGT 120
 Db 80 ADGVKGRFTISRDNKNTLYLQNMNSLRADPTAVYCAKRR-KAVRGISRYNYMDVMGKGT 132
 QY 121 TVTVSS 125

Db 133 ITVSS 137

RESULT 14

Q9UL91 PRELIMINARY; PRT; 118 AA.

AC Q9UL91; DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP: P01772; 2F84.
DR InterPro: IPR007110; Ig-1ike.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1 118
FT SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 63.3%; Score 423.5; DB 4; Length 118;

Best Local Similarity 64.5%; Pred. No. 5e-37; Mismatches 20; Indels 7; Gaps 1;

Matches 80; Conservative 17; Indels 7; Gaps 1;

QY 1 QVLLSGGGVVOPGGSLRVACVAGFTFRNFGMHVROAPGKGLWVAFIWPDASNKGY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYNNMWRQAPGKGLEWVSYSITITYY 60
QY 61 GDSYKGRFTVSRDPSKNTLYIQNGILRAEDTAVYGCAREKAVRGISRYNYMDVWGKGT 120
DB 61 ADSYKGRFTISRDNKSLYLQNNSLRAEDTAVYGCAREKAVRGISRYNYMDVWGKGT 113
QY 121 TVTVSS 124
DB 114 TVTVSS 117

RESULT 15

Q9UL72 PRELIMINARY; PRT; 118 AA.

AC Q9UL72; DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035042; AAD56278.1; -.
DR HSSP: P01772; 2F84.
DR InterPro: IPR007110; Ig-1ike.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1 118
FT SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 60.0%; Score 401.5; DB 4; Length 118;

Best Local Similarity 63.5%; Pred. No. 1.1e-34; Mismatches 19; Indels 9; Gaps 3;

Matches 80; Conservative 18; Mismatches 19; Indels 9; Gaps 3;

QY 1 QVLLSGGGVVOPGGSLRVACVAGFTFRNFGMHVROAPGKGLWVAFIWPDASNKGY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYNNMWRQAPGKGLEWVSYSITITYY 59
QY 61 GDSYKGRFTVSRDPSKNTLYIQNGILRAEDTAVYGCAREKAVRGISRYNYMDVWGKGT 119
DB 60 ADSYKGRFTISRDNKSLYLQNNSLRAEDTAVYGCAREKAVRGISRYNYMDVWGKGT 112
QY 120 TVTVSS 125
DB 113 TVTVSS 118

Search completed: January 22, 2004, 11:53:09
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:37:35 ; Search time 39.1304 Seconds
(without alignments)
507.043 Million cell updates/sec

Title: US-09-147-443d-58

Perfect score: 669

Sequence: 1 QVTLKSGGVVPGSGSLRV.....SRNYMDWKGKTTVSS 125

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669	100.0	125	19	AAW52232
2	669	100.0	125	19	AAW52240
3	669	100.0	125	19	AAW52242
4	623	93.1	125	19	AAW52234
5	615	91.9	125	19	AAW52236
6	615	91.9	125	19	AAW52226
7	611	89.8	125	19	AAW52222
8	600.5	88.2	125	19	AAW52228
9	590	88.2	125	19	AAW52218

10	575.5	86.0	126	19	AAW52220	Antibody LD1-117-V
11	575	85.9	125	19	AAW52212	Antibody LD1-40-VH
12	569	85.1	125	19	AAW52230	Antibody LD2-11-VH
13	569	85.1	125	19	AAW52224	Antibody LD2-4-VH
14	569	85.1	125	19	AAW52216	Antibody LD1-84-VH
15	564	84.3	125	19	AAW52214	Antibody LD1-52-VH
16	543.5	81.2	126	22	AAW52210	Human anti-Rh(D) a
17	543	81.2	125	22	AAW52208	Human anti-Rh(D) c
18	543	81.2	125	22	AAW52206	Human anti-Rh(D) c
19	543	81.2	125	22	AAW52204	Human anti-Rh(D) c
20	543	81.2	125	22	AAW52202	Human anti-Rh(D) c
21	542.5	81.1	126	22	AAW52200	Human anti-Rh(D) c
22	541.5	80.9	126	22	AAW52198	Human anti-Rh(D) c
23	541.5	80.9	126	22	AAW52196	Human anti-Rh(D) c
24	541.5	80.9	126	22	AAW52194	Human anti-Rh(D) c
25	541.5	80.9	126	22	AAW52192	Human anti-Rh(D) c
26	539.5	80.6	126	22	AAW52190	Human anti-Rh(D) c
27	535	80.0	125	22	AAW52188	Human anti-Rh(D) c
28	533	79.7	127	22	AAW52186	Human anti-Rh(D) a
29	530	79.2	127	22	AAW52184	Human anti-Rh(D) a
30	528	78.9	125	22	AAW52182	Human anti-Rh(D) c
31	528	78.9	125	22	AAW52180	Human anti-Rh(D) c
32	527	78.8	125	22	AAW52178	Human anti-Rh(D) c
33	526.5	78.7	126	22	AAW52176	Human anti-Rh(D) c
34	524	78.3	127	22	AAW52174	Human anti-Rh(D) c
35	522.5	78.1	128	19	AAW52172	Human anti-Rh(D) c
36	520.5	77.8	126	22	AAW52170	Human anti-Rh(D) c
37	519	77.6	127	22	AAW52168	Human anti-Rh(D) c
38	518.5	77.5	126	22	AAW52166	Human anti-Rh(D) c
39	518.5	77.5	126	22	AAW52164	Human anti-Rh(D) c
40	517.5	77.4	126	22	AAW52162	Human anti-Rh(D) a
41	517.5	77.4	143	21	AAW52160	Human PTHrP monocl
42	517.5	77.4	143	21	AAW52158	Human PTHrP monocl
43	516	77.1	146	23	AAW52156	Human recombinant
44	512.5	76.6	477	22	AAU14288	Human novel protei
45	510.5	76.3	143	21	AAV82621	Human PTHrP monocl

ALIGNMENTS

RESULT 1
ID AAW52232 standard; Protein; 125 AA.
AC AAW52232:
XX
XX 12-JUN-1998 (first entry)
XX
XX
XX Antibody LD2-14-VH chain sequence.
DE
XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN therapy;
KW Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
XX Homo sapiens.
XX
XX WO9749809-A1.
XX
XX 31-DEC-1997.
XX
XX 20-JUN-1997; 97WO-EP03253.
XX
XX 24-JUN-1996; 96EP-0810421.
XX
XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB ELUTSPENDE.
XX
XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
XX Vogel M;
XX WFI, 1998-077173/07.
XX N-PSDB; AAV19756.
XX

PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
XX
XX
PS Claim 1, Fig 11A; 68pp; English.
XX
CC This sequence is the antibody LD2-14-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 669; DB 19; Length 125;
Best Local Similarity 100.0%; Pred. No. 5,1e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKGLBWAFTWPDASNKGY 60
DB 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKGLBWAFTWPDASNKGY 60
QY 61 GDSVKGRFTVSRDNSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 GDSVKGRFTVSRDNSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
QY 121 VTWSS 125
DB 121 VTWSS 125
RESULT 2
AAW52240
ID AAW52240 standard; Protein; 125 AA.
XX
AC AAW52240;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD1/2-6-3-VH chain sequence.
XX
KM Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
EN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
DR WPI; 1998-077173/07.
DR N-PSDB; AAV19764.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise

PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
XX
XX
PS Claim 1, Fig 15A; 68pp; English.
XX
CC This sequence is the antibody LD1/2-6-3-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 669; DB 19; Length 125;
Best Local Similarity 100.0%; Pred. No. 5,1e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKGLBWAFTWPDASNKGY 60
DB 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKGLBWAFTWPDASNKGY 60
QY 61 GDSVKGRFTVSRDNSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 GDSVKGRFTVSRDNSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
QY 121 VTWSS 125
DB 121 VTWSS 125
RESULT 3
AAW52242
ID AAW52242 standard; Protein; 125 AA.
XX
AC AAW52242;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD1/2-6-33-VH chain sequence.
XX
KM Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
EN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
DR WPI; 1998-077173/07.
DR N-PSDB; AAV19764.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic

PT thrombocytopenic purpura
 XX
 PS Claim 1, Fig 16A; 68pp; English.
 XX
 CC This sequence is the antibody LD1/2-6-33-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.
 CC
 SQ Sequence 125 AA;
 Query Match 100.0%; Score 669; DB 19; Length 125;
 Best Local Similarity 100.0%; Pred. No. 5.1e-55;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVLTLESGGGVWPQGSILRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIWFDSNKG 60
 DB 1 QVLTLESGGGVWPQGSILRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIWFDSNKG 60
 QY 61 GDSVKGKFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
 DB 61 GDSVKGKFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
 QY 121 VTVSS 125
 DB 121 VTVSS 125
 RESULT 4
 AAM52234
 ID AAM52234 standard; Protein; 125 AA.
 AC AAM52234;
 XX
 DT 12-JUN-1998 (first entry)
 DE Antibody LD2-17-VH chain sequence.
 XX
 DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
 XX
 OS Homo sapiens.
 OS
 PN MO9749809-A1.
 PN
 PD 31-DEC-1997.
 XX
 PF 20-JUN-1997; 97WO-EP03253.
 XX
 PR 24-JUN-1996; 96EP-0810421.
 XX
 PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
 XX
 PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
 PI Vogel M;
 DR WPI; 1998-077173/07.
 DR N-PSDB; AAV19758.
 PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic
 PT thrombocytopenic purpura

XX
 PS Claim 1, Fig 12A; 68pp; English.
 XX
 CC This sequence is the antibody LD2-17-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.
 CC
 SQ Sequence 125 AA;
 Query Match 93.1%; Score 623; DB 19; Length 125;
 Best Local Similarity 91.2%; Pred. No. 1e-50;
 Matches 114; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QVLTLESGGGVWPQGSILRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIWFDSNKG 60
 DB 1 QVLTLESGGGVWPQGSILRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIWFDSNKG 60
 QY 61 GDSVKGKFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
 DB 61 VDSVKGKFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
 QY 121 VTVSS 125
 DB 121 VTVSS 125
 RESULT 5
 AAM52236
 ID AAM52236 standard; Protein; 125 AA.
 AC AAM52236;
 XX
 DT 12-JUN-1998 (first entry)
 DE Antibody LD2-20-VH chain sequence.
 XX
 DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
 XX
 OS Homo sapiens.
 OS
 PN MO9749809-A1.
 PN
 PD 31-DEC-1997.
 XX
 PF 20-JUN-1997; 97WO-EP03253.
 XX
 PR 24-JUN-1996; 96EP-0810421.
 XX
 PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
 XX
 PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
 PI Vogel M;
 DR WPI; 1998-077173/07.
 DR N-PSDB; AAV19760.
 PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic
 PT thrombocytopenic purpura

PS Claim 1; Fig 13A; 68bp; English.

CC This sequence is the antibody LD2-20-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after transfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 91.9%; Score 615; DB 19; Length 125;
Best Local Similarity 90.4%; Pred. No. 5,6e-50;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLLESQGGVVPQGSILRVACVAGSFTFRNFGMHVROAPGKGLRWVAFIWPDSNKG 60
DB 1 QVQLLESQGGVVPQGSILRVACVAGSFTFRNFGMHVROAPGKGLRWVAFIWPDSNKG 60

QY 61 GDSVKGRTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDWGKGT 120
DB 61 VDSVKGRTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKALRGISRYNYLDWGKGT 120

QY 121 VTIVSS 125
DB 121 VTIVSS 125

RESULT 6
AAW52226
ID AAW52226 standard; Protein; 125 AA.

XX AAW52226;

DT 12-JUN-1998 (first entry)

XX Antibody LD2-5-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX Homo sapiens.

XX WO9749809-A1.

XX 31-DEC-1997.

XX 20-JUN-1997; 97WO-EP03253.

XX 24-JUN-1996; 96EP-0810421.

XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;

XX WPI; 1998-077173/07.

XX N-PSDB; AAV19750.

XX New Rhesus D antigen binding polypeptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura

XX Claim 1; Fig 8A; 68bp; English.

PS

XX This sequence is the antibody LD2-5-VH chain sequence, which is a

CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after transfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 91.9%; Score 615; DB 19; Length 125;
Best Local Similarity 89.6%; Pred. No. 5,6e-50;
Matches 112; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLLESQGGVVPQGSILRVACVAGSFTFRNFGMHVROAPGKGLRWVAFIWPDSNKG 60
DB 1 QVQLLESQGGVVPQGSILRVACVAGSFTFRNFGMHVROAPGKGLRWVAFIWPDSNKG 60

QY 61 GDSVKGRTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDWGKGT 120
DB 61 VDSVKGRTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKALRGISRYNYLDWGKGT 120

QY 121 VTIVSS 125
DB 121 VTIVSS 125

RESULT 7
AAW52222
ID AAW52222 standard; Protein; 125 AA.

XX AAW52222;

DT 12-JUN-1998 (first entry)

XX Antibody LD2-1-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX Homo sapiens.

XX WO9749809-A1.

XX 31-DEC-1997.

XX 20-JUN-1997; 97WO-EP03253.

XX 24-JUN-1996; 96EP-0810421.

XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;

XX WPI; 1998-077173/07.

XX N-PSDB; AAV19746.

XX New Rhesus D antigen binding polypeptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura

XX Claim 1; Fig 6A; 68bp; English.

PS

CC This sequence is the antibody LD2-1-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after transfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

SO Sequence 125 AA;

Query Match 91.3%; Score 611; DB 19; Length 125;
Best Local Similarity 88.8%; Pred. No. 1.3e-49;
Matches 111; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVTLSSGGGVVPGGSLRVACVAGFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKGK 60
DB 1 QVTLSSGGGVVPGGSLRVACVAGFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKGK 60
QY 61 GDSVKGRTVSRDNRKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 VDSVKGRTVSRDNRKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
QY 121 TVTVSS 125
DB 121 TVTVSS 125

RESULT 8
AAW52228
ID AAW52228 standard; Protein; 126 AA.

AAW52228;

12-JUN-1998 (first entry)

Antibody LD2-10-VH chain sequence.

Antibody; variable heavy chain; VH chain; variable light chain; VL chain;

Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

Homo sapiens.

MO9749809-A1.

31-DEC-1997.

20-JUN-1997; 97WO-EP03253.

24-JUN-1996; 96EP-0810421.

(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

WPI, 1998-077173/07.

New Rhesus D antigen binding poly:peptide(s) - used to neutralise

Rhesus D antigen in therapy, e.g. for treating idiopathic

thrombocytopenic purpura

Claim 1; Fig 9A; 68pp; English.

This sequence is the antibody LD2-10-VH chain sequence, which is a

CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after transfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

SO Sequence 126 AA;

Query Match 89.8%; Score 600.5; DB 19; Length 126;
Best Local Similarity 88.1%; Pred. No. 1.3e-48;
Matches 111; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVTLSSGGGVVPGGSLRVACVAGFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKGK 60
DB 1 QVTLSSGGGVVPGGSLRVACVAGFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKGK 60
QY 61 GDSVKGRTVSRDNRKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 119
DB 61 VDSVKGRTVSRDNRKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 9
AAW52218
ID AAW52218 standard; Protein; 125 AA.

AAW52218;

12-JUN-1998 (first entry)

Antibody LD1-110-VH chain sequence.

Antibody; variable heavy chain; VH chain; variable light chain; VL chain;

Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

Homo sapiens.

MO9749809-A1.

31-DEC-1997.

20-JUN-1997; 97WO-EP03253.

24-JUN-1996; 96EP-0810421.

(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

WPI, 1998-077173/07.

New Rhesus D antigen binding poly:peptide(s) - used to neutralise

Rhesus D antigen in therapy, e.g. for treating idiopathic

thrombocytopenic purpura

Claim 1; Fig 4A; 68pp; English.

This sequence is the antibody LD1-110-VH chain sequence, which is a

polypeptide of the invention. The polypeptides are capable of forming

CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

SQ Sequence 125 AA;

Query Match 88.2%; Score 590; DB 19; Length 125;

Best Local Similarity 85.6%; Pred. No. 1.2e-47;

Matches 107; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVLLSGGGVVPQGSILRVACVAGFTFRNFGMHVROAPGKLEWVAFIWPDAENKGY 60
DB 1 QVLLSGGGVVPQGSILRVACVAGFTFRNFGMHVROAPGKLEWVAFIWPDAENKGY 60
QY 61 GDSVKGKFTVSRDNRKNTLYLQWNGLRABDTAVYYCARERAVRGIISRYNYMDVWGKGT 120
DB 61 ADSVKGKFTVSRDNRKNTLYLQWNGLRABDTAVYYCARERAVRGIISRYNYMDVWGKGT 120
QY 121 VTWSS 125
DB 121 VTWSS 125

RESULT 10

AAW52220 standard; Protein; 126 AA.

AAW52220;

12-JUN-1998 (first entry)

Antibody LD1-117-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

Homo sapiens.

MO9749809-A1.

31-DEC-1997.

20-JUN-1997; 97WO-EP03253.

24-JUN-1996; 96EP-0810421.

(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

WPI; 1998-077173/07.

N-PSDB; AAV19744.

XX New Rhesus D antigen binding poly:peptide(s) - used to neutralise
XX Rhesus D antigen in therapy, e.g. for treating idiopathic
XX thrombocytopenic purpura

Claim 1; Fig 5A; 68pp; English.

XX This sequence is the antibody LD1-117-VH chain sequence, which is a
XX polypeptide of the invention. The polypeptides are capable of forming
XX antigen binding structures with specificity for Rhesus D antigens which

CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

SQ Sequence 126 AA;

Query Match 86.0%; Score 575.5; DB 19; Length 126;

Best Local Similarity 84.9%; Pred. No. 2.8e-46;

Matches 107; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVLLSGGGVVPQGSILRVACVAGFTFRNFGMHVROAPGKLEWVAFIWPDAENKGY 60
DB 1 QVLLSGGGVVPQGSILRVACVAGFTFRNFGMHVROAPGKLEWVAFIWPDAENKGY 60
QY 61 GDSVKGKFTVSRDNRKNTLYLQWNGLRABDTAVYYCARERAVRGIISRYNYMDVWGKGT 119
DB 61 ADSVKGKFTVSRDNRKNTLYLQWNGLRABDTAVYYCARERAVRGIISRYNYMDVWGKGT 120
QY 120 TWTWSS 125
DB 121 TWTWSS 126

RESULT 11

AAW52212 standard; Protein; 125 AA.

AAW52212;

12-JUN-1998 (first entry)

Antibody LD1-40-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

Homo sapiens.

MO9749809-A1.

31-DEC-1997.

20-JUN-1997; 97WO-EP03253.

24-JUN-1996; 96EP-0810421.

(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

WPI; 1998-077173/07.

N-PSDB; AAV19736.

XX New Rhesus D antigen binding poly:peptide(s) - used to neutralise
XX Rhesus D antigen in therapy, e.g. for treating idiopathic
XX thrombocytopenic purpura

Claim 1; Fig 1A; 68pp; English.

XX This sequence is the antibody LD1-40-VH chain sequence, which is a
XX polypeptide of the invention. The polypeptides are capable of forming
XX antigen binding structures with specificity for Rhesus D antigens which
XX include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of

CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN). In subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 85.9%; Score 575; DB 19; Length 125;
 Best Local Similarity 84.7%; Pred. No. 3e-46;
 Matches 105; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIWFDSNKG 60
 DB 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIWFDSNKG 60
 QY 61 GDSVKGFTVSRNRSKNTLYLQWNGLRADPTAVYYCARERAVRGISRYNYMDVWGKGT 120
 DB 61 GDSVKGFTVSRNRSKNTLYLQWNGLRADPTAVYYCARERAVRGISRYNYMDVWGKGT 120
 QY 121 VTYS 124
 DB 121 VTYS 124

RESULT 12

AAW52230 standard; Protein; 125 AA.

XX AAW52230;

XX 12-JUN-1998 (first entry)

XX Antibody LD2-11-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;

XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX Homo sapiens.

XX WO9749809-A1.

XX 31-DEC-1997.

XX 20-JUN-1997; 97WO-EP03253.

XX 24-JUN-1996; 96EP-0810421.

XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

XX Vogel M;

XX MPI; 1998-077173/07.

XX N-PSDB; AAV19754.

XX New Rhesus D antigen binding poly:peptide(s) - used to neutralise

XX Rhesus D antigen in therapy, e.g. for treating idiopathic

XX thrombocytopenic purpura

XX Claim 1; Fig 10A; 68pp; English.

CC This sequence is the antibody LD2-11-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The

CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN). In subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 85.1%; Score 569; DB 19; Length 125;
 Best Local Similarity 84.0%; Pred. No. 1.1e-45;
 Matches 105; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIWFDSNKG 60
 DB 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIWFDSNKG 60
 QY 61 GDSVKGFTVSRNRSKNTLYLQWNGLRADPTAVYYCARERAVRGISRYNYMDVWGKGT 120
 DB 61 GDSVKGFTVSRNRSKNTLYLQWNGLRADPTAVYYCARERAVRGISRYNYMDVWGKGT 120
 QY 121 VTYS 125
 DB 121 VTYS 125

RESULT 13

AAW52224 standard; Protein; 125 AA.

XX AAW52224;

XX 12-JUN-1998 (first entry)

XX Antibody LD2-4-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;

XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX Homo sapiens.

XX WO9749809-A1.

XX 31-DEC-1997.

XX 20-JUN-1997; 97WO-EP03253.

XX 24-JUN-1996; 96EP-0810421.

XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

XX Vogel M;

XX MPI; 1998-077173/07.

XX N-PSDB; AAV19748.

XX New Rhesus D antigen binding poly:peptide(s) - used to neutralise

XX Rhesus D antigen in therapy, e.g. for treating idiopathic

XX thrombocytopenic purpura

XX Claim 1; Fig 7A; 68pp; English.

CC This sequence is the antibody LD2-4-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for

CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 85.1%; Score 569; DB 19; Length 125;
Best Local Similarity 84.0%; Pred. No. 1.1e-45;
Matches 105; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 1 QVTLSEGGGVVPGGSLRVAACVAGSFTFRNFGMHWROAPGKGLRVAFTWPDASNKGY 60
DB 1 QVTLSEGGGVVPGGSLRSLSCASGFTLRSSGMHWROAPGKGLRVAFTWPDGSIKSY 60
QY 61 GDSVKGKFTVSRDNRKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 AESVKGKFTISRDTSKNTLYLQNRSLADDTAVYYCARDKAVRGISRYNYMDVWGKGT 120
QY 121 VTWSS 125
DB 121 VTWSS 125

RESULT 14
AAW52216
ID AAW52216 standard; Protein; 125 AA.
XX
AC AAW52216;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD1-84-VH chain sequence.
XX
KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
PN MO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
DR WPI; 1998-077173/07.
XX
DR N-PSDB; AAV19740.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
XX
PS Claim 1, Fig 3A; 68pp; English.
XX
CC This sequence is the antibody LD1-84-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,

CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 85.1%; Score 569; DB 19; Length 125;
Best Local Similarity 84.0%; Pred. No. 1.1e-45;
Matches 105; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 1 QVTLSEGGGVVPGGSLRVAACVAGSFTFRNFGMHWROAPGKGLRVAFTWPDASNKGY 60
DB 1 QVTLSEGGGVVPGGSLRSLSCASGFTLRSSGMHWROAPGKGLRVAFTWPDGSIKSY 60
QY 61 GDSVKGKFTVSRDNRKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 AESVKGKFTISRDTSKNTLYLQNRSLADDTAVYYCARDKAVRGISRYNYMDVWGKGT 120
QY 121 VTWSS 125
DB 121 VTWSS 125

RESULT 15
AAW52214
ID AAW52214 standard; Protein; 125 AA.
XX
AC AAW52214;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD1-52-VH chain sequence.
XX
KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
PN MO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
DR WPI; 1998-077173/07.
XX
DR N-PSDB; AAV19738.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
XX
PS Claim 1, Fig 2A; 68pp; English.
XX
CC This sequence is the antibody LD1-52-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the

CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX

SQ Sequence 125 AA;

Query Match 84.3%; Score 564; DB 19; Length 125;

Best Local Similarity 83.2%; Pred. No. 3.2e-45;

Matches 104; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVRLSSGGGVOPGSGIRVACVAGFTFNNFGMHWVROAPGKLEWVAFIMFDASNKGY 60
Db 1 QVRLSSGGGVOPGSGIRLSCASGPAIRSSGMHWVROAPGKLEWVAFIMFDGSIKSY 60
QY 61 GDSVKGKRFIVSRDINSKNTLYLQWNGLRADPTAVYYCAREKAVRGISRYNYMDVWGKGT 120
Db 61 AESSVKGKRFITSRDTSKNTLYLQWRSLSADDTAVYYCARDKAVRGISRYNYMDVWGKGT 120
QY 121 VTVSS 125
Db 121 VTVSS 125

Search completed: January 22, 2004, 11:51:20
Job time : 40.1304 secs

Db 121 TVSVSS 126

RESULT 2
US-09-848-798-8

: APPLICANT : Siegel, Donald L.
 : TITLE OF INVENTION : Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLULED
 : TITLE OF INVENTION : SORTING METHOD FOR PRODUCTION THEREOF
 : FILE REFERENCE : 09596-4202
 : CURRENT APPLICATION NUMBER : US/09/848,798

OTHER INFORMATION: anti-Rh(D) chain D01
US-09-848-798-8

Query Match	81.2%	Score 543	DB 11	length 125
Best Local Similarity	80.0%	Pred. No. 1.8e-43		
Matches 100, Conservative	9	Mismatches 16	Indels 0	Gaps 0

[illegible]

QY	121	VT	VSS	125
Db	121	VT	VSS	125

RESULT 3
US-09-848-798-20

: APPLICANT: Siegel, Donald L.
 : TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLULAR
 : TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 : FILE REFERENCE: 09596-4202
 : CURRENT APPLICATION NUMBER: US/09/848,798

OTHER INFORMATION: anti-Rh(D) chain D15
US-09-848-798-20

Query Match	81.2%;	Score 543;	DB 11;	Length 125;
Best Local Similarity	80.0%;	Pred. No. 1.8e-43;		

Matches 100; Conservative 9; Mismatches 16; Indels 0; Gaps 0.

Dy 1 QVLLIESGGGVQPGSLRVCVASGTFRNFGMHWQAQPKGLEBWAFLWFEDASNKGY
:
Db 1 EYGLLESGGGVQPGSRLRCSCVSGFTFNMYGMHWQAQPKGLEBWAAVLWFDGSNKKYY

```

Oy      61 GDSVKGRFLVSRDNSKNTLYLQNGGLRAEDTAVVYICAREKAVRGISRIYNYMDWGKCTT 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKGRFTISRDNKNTLYLQNMSSLRADETAVVYICARENGIKLWSRYLYFYDYGQGTLL 120

```

QY	121	VTVSS	125
Db	121	VTVSS	125

RESULT 4
US-09-848-798-21
; Sequence 21, Application US/09848798
; Publication No. US20030040605A1

1 TITLE Applicant: Siegel, Donald L.
2 TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLULAR
3 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
4 FILE REFERENCE: 09596-4202
5 CURRENT APPLICATION NUMBER: US/09/848,798
6 CURRENT FILING DATE: 2001-05-04
7 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
8 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
9 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
10 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
11 NUMBER OF SEQ ID NOS: 224
12 SOFTWARE: PatentIn Ver. 2.0

OTHER INFORMATION: anti-Rh(D) chain D16
US-09-848-798-21

Query Match	81.2%	Score 543	DB 11	Length 125
Best Local Similarity	80.0%	Pred. No. 1.8e-43		
Matches 100	Conservative	9	Mismatches 16	Indels 0
				Gaps 0

Dy 1 QVKLTESGGGVQPGGSLRVACVAGSGTFRNGMHWVRQAPEGKLEWVAIFWFDASNKGK 60
 : ::::| | | | | | | | | | | | | | | | |
Db 1 EVQLLESGGGVQPGRSLRLSCVSGFTFNNGMHWRQAPEGKLEWVAIWFDASNKKY 60

```
Qy      61 GDSYKGRFFVSRDNSKNTLYLQNMGLRAEDTAVVYICAREKAVRGISRYNYIWDVWGKGT 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSYKGRFFVSRDNSKNTLYLQNMGLRAEDTAVVYICARENGIKLWGRYLYYFDYWGQGT 120
```

QY	121	VTVSS	125
Db	121	VTVSS	125

RESULT 5
US-09-848-798-22
; Sequence 22, Application US/09848798
; Publication No. US20030040605A1

1 APPLICANT Siegel, Donald L.
 2 TITLE OF INVENTION: (S/D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 3 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 4 FILE REFERENCE: 09596-4202
 5 CURRENT APPLICATION NUMBER: US/09/848,798
 6 CURRENT FILING DATE: 2001-05-04
 7 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
 8 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
 9 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
 10 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
 11 NUMBER OF SEQ ID NOS: 224

```
US-09-848-798-22
Query Match      81.2%; Score 543; DB 11; Length 125;
Best Local Similarity 80.0%; Pred. No. 2, 1e-43;
Matches 100; Conservative 9; Mismatches 16; Indels 0; Gaps 0

QY 1 QVKLLSEGGGVQPFGSLRVACVAGGFTFRNGEMHWVRQAPGKGLFWAFIFPDASNKCY 60
   :::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 1 EVQLLESGGCVVQPGPSRLRSCVSGGFITFNNGMHWVRQAPGKGLFWAVIWFDSGNKKY 60

QY 61 GDSVYGRFTVSRDNSKNITYLQMNGLRADDTAVYYCARGLRSRYNYMDVGSKGT 120
   :::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 61 ADSVYGRFTISRDNSTNTLYLQMNSLRADDTAVYYCARENQIKLSRIYLIDYMGQGIT 120

QY 121 TVTSS 125
   ||||
DB 121 TVTSS 125

RESULT 6
US-09-848-798-17
Sequence 17, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848, 798
PRIORITY FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D12
US-09-848-798-17

Query Match      81.1%; Score 542.5; DB 11; Length 126;
Best Local Similarity 80.2%; Pred. No. 2, 1e-43;
Matches 101; Conservative 12; Mismatches 12; Indels 1; Gaps 1

QY 1 QVKLLSEGGGVQPGSILRVACVASGFTFRNFGMHWRQAPGKGLFWAFIFPDASNKCY 60
   :::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 1 EVQLLESGGCVVQPGPSRLRLCAASGFSFPRSYGMHWRQAPGKGLFWAFIWFDSGNKKY 60

QY 61 GDSVYGRFTVSRDNSKNITYLQMNGLRADDTAVYYCARERKA-VRGISRRNYIMDVGSKGT 119
   :::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 61 VDSVYGRFTISRDNSTNTLYLEMNSLRVDITAVYYCARASMLRGISRYTYAMDVGPGT 120

QY 120 TVTSS 125
   ||||
DB 121 TVTSS 126

RESULT 7
US-09-848-798-14
Sequence 14, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
```

```

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D10
US-09-848-798-15

Query Match      80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1

1 QVLLSEGGGVVQGGSLRIVACVSGFFRRFGMHMWQAQPGKGLEWVAFIFDASNKGY 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 EVLLSEGGGVVQGGSLRILSCASKFTLYNYGMHWQAQPGKGLEWVAFIFDGSNKTY 60
GDSVKGRTVSRRDSKNTLYLQNNGLRAEDTAVVYCAEKGAVR-GISRYNMYMDWGKGT 119
61 EDVSKGRFTVSRRDSKNTLYLQNNSLRAEDTAVVYCAEKGSKVALSRYYMDWGQGT 120

RESULT 8
US-09-848-798-15
Sequence 15, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D10
US-09-848-798-15

Query Match      80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1

1 QVLLSEGGGVVQGGSLRIVACVSGFFRRFGMHMWQAQPGKGLEWVAFIFDASNKGY 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 EVLLSEGGGVVQGGSLRILSCASKFTLYNYGMHWQAQPGKGLEWVAFIFDGSNKTY 60
GDSVKGRTVSRRDSKNTLYLQNNGLRAEDTAVVYCAEKGAVR-GISRYNMYMDWGKGT 119
61 EDVSKGRFTVSRRDSKNTLYLQNNSLRAEDTAVVYCAEKGSKVALSRYYMDWGQGT 120

```

QY 120 TTTVSS 125
121 TTTVSS 126

RESULT 9

US-09-848-798-147
; Sequence 147, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 147
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH32
US-09-848-798-147

Query Match 80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVTLSEGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWPDASNKGY 60
1 EVQLLESGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWPDASNKGY 60
Db 61 GDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 119
61 EDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 120

QY 120 TTTVSS 125
121 TTTVSS 126

RESULT 10

US-09-848-798-148
; Sequence 148, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 148
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH37
US-09-848-798-148

Query Match 80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVTLSEGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWPDASNKGY 60
1 EVQLLESGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWPDASNKGY 60
Db 61 GDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 119
61 EDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 120

QY 120 TTTVSS 125
121 TTTVSS 126

RESULT 11

US-09-848-798-16
; Sequence 16, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D11
US-09-848-798-16

Query Match 80.6%; Score 539.5; DB 11; Length 126;
Best Local Similarity 81.0%; Pred. No. 4e-43;
Matches 102; Conservative 10; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVTLSEGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWPDASNKGY 60
1 EVQLLESGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWPDASNKGY 60
Db 61 GDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 119
61 EDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 120

QY 120 TTTVSS 125
121 TTTVSS 126

RESULT 12

US-09-848-798-23
; Sequence 23, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
US-09-848-798-23


```

US-09-848-798-145
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/848,798
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ. ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 145
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH25
US-09-848-798-145

Query Match          79.2%; Score 530; DB 11; Length 127;
Best Local Similarity 79.5%; Pred. No. 3.1e-42;
Matches 101; Conservative 11; Mismatches 13; Indels 2; Gaps 2

QY      1 QVQLL-ESGGGVAVQPGSLRVAQCVASGTFTRNFGMHWROAPGKGLEWVAFIWPDASNKG 59
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      1 EYQLLEESGGGVAVQPGSLRLTILCAASGSPFSYGMHWROAPGKGLEWVAFTWPDGSKNY 60
        YDVSVGRFTVSRDINSKNTLYIQNMNGLAEDTAVYVYCAR- KAVRGISRYNYVDWVGK 118
        |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
        61 YDVSVGRFTVSRDINSKNTLYIQNMNGLAEDTAVYVYCAR- KAVRGISRYNYVDWVGK 120

QY      119 TTVTVSS 125
        |||||
DB      121 TTVTVSS 127

RESULT 15
US-09-848-798-9
Sequence 9, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/848,798
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ. ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D03
US-09-848-798-9

Query Match          78.9%; Score 528; DB 11; Length 125;
Best Local Similarity 78.4%; Pred. No. 4.7e-42;
Matches 98; Conservative 10; Mismatches 17; Indels 0; Gaps 0

QY      1 QVQLLESGGGVAVQPGSLRVAQCVASGTFTRNFGMHWROAPGKGLEWVAFIWPDASNKG 60
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      1 EYQLLEESGGGVAVQPGSLRLTILCAASGTFSTYGMHWROAPGKGLEWVAFTWPDGSKNY 60
        YDVSVGRFTVSRDINSKNTLYIQNMNGLAEDTAVYVYCAR- KAVRGISRYNYVDWVGK 120

```

Db	61	ADSVKGRFTVSRDNRKNTLYLQWNSLRAPDTAVVYCAREEVVRGVILMSRKFDTWQCTL	120
Qy	121	VTWSS	125
Db	121	VTWSS	125

Search completed: January 22, 2004, 12:00:41
Job time : 38.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:44:30 ; Search time 14.1522 Seconds
(without alignments)
713.510 Million cell updates/sec

Title: US-09-147-443D-60

Perfect score: 543

Sequence: 1 VMTQSPSSLSASVGDRVTIT.....CQGSYTPYTFGGQTKLQIK 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	89.7	109	2	S31981 Ig kappa chain - h
2	486	89.5	127	2	S40367 Ig kappa chain V-J
3	483	89.0	109	2	S31998 Ig kappa chain - h
4	482	88.8	123	2	S40331 Ig kappa chain - h
5	476	87.7	108	2	B49047 Ig kappa chain V r
6	474	87.3	109	2	S31978 Ig kappa chain - h
7	472	86.9	108	2	S47182 Ig kappa chain - h
8	465	85.6	108	2	S44122 Ig kappa chain V r
9	461	84.9	109	2	S31979 Ig kappa chain - h
10	460	84.7	108	2	S31977 Ig kappa chain - h
11	459	84.5	129	2	S52793 Ig kappa chain V r
12	458	84.3	129	1	K1HUK Ig kappa chain pre
13	457	84.2	108	1	K1HUB Ig kappa chain V-I
14	457	84.2	109	2	S31980 Ig kappa chain - h
15	456	84.0	108	2	S19674 Ig kappa chain V r
16	456	84.0	129	2	S40317 Ig kappa chain - h
17	454	83.6	122	2	S40314 Ig kappa chain - h
18	452	83.2	107	2	K16264 Ig lambda chain V
19	452	83.2	108	1	K1HUB Ig kappa chain V-I
20	452	83.2	122	2	S40370 Ig kappa chain - h
21	449	82.7	129	2	S52792 Ig kappa chain V r
22	448	82.5	109	2	S32001 Ig kappa chain - h
23	448	82.5	120	2	S46370 Ig kappa chain V-J
24	447	82.3	108	1	K1HUB Ig kappa chain V-I
25	445	82.0	109	2	S31983 Ig kappa chain - h
26	442	81.4	109	2	UN0286 Ig kappa chain V-J
27	440	81.0	117	2	S46371 Ig kappa chain V-J
28	438.5	80.8	125	2	S40315 Ig kappa chain - h
29	437.5	80.6	107	2	S36275 Ig lambda chain V

30	437	80.5	125	2	S40333 Ig kappa chain V-J
31	435	80.1	129	2	S40369 Ig kappa chain - h
32	434	79.9	108	1	K1HOU Ig kappa chain V-I
33	434	79.9	117	2	S24206 Ig kappa chain V r
34	433	79.7	125	2	S40350 Ig kappa chain - h
35	433	79.7	128	2	S46372 Ig kappa chain var
36	432	79.6	126	2	S52789 Ig kappa chain V r
37	432	79.6	129	2	S40335 Ig kappa chain V r
38	431	79.4	107	2	JL0139 Ig kappa chain V r
39	431	79.4	108	1	K1HUB Ig kappa chain V-I
40	430.5	79.3	106	2	PC2397 anti-tetanus toxin
41	430.5	79.3	109	1	K1HUB Ig kappa chain V-I
42	430	79.2	107	1	S36262 Ig lambda chain V
43	430	79.2	125	2	S40349 Ig kappa chain V-J
44	429	79.0	107	2	S36269 Ig lambda chain V
45	428	78.8	132	2	S38646 Ig kappa chain V r

ALIGNMENTS

RESULT 1

S31981
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31981
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31981
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <FOR>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMV>

Query Match 89.7%; Score 487; DB 2; Length 109;
Best Local Similarity 88.6%; Pred. No. 2.6e-36;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRVTITCRASQSIIRYIMWYOHKPKAPKLIHTASSLSQGVSPRF 60
DB 3 VMTQSPSSLSASVGDRVTITCRASQDISRYIMWYOHKPKAPKLIHTASSLSQGVSPRF 62
QY 61 SGSGSGTDFLTITSSLPDPFATYYCQGSYTPYTFGGQTKLQIK 105
DB 63 SGSGSGTDFLTITSSLPDPFATYYCQGSYTPYTFGGQTKLQIK 107

RESULT 2

S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 15-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MIMD:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <ILV>
A/Cross-references: EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMV>

Query Match 89.5%; Score 486; DB 2; Length 127;

Best Local Similarity 90.4%; Pred. No. 3.7e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 61
DB 21 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 80

QY 62 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 81 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 124

RESULT 3
S31998
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31998
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31998
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <PDR>
A/Cross-references: EMBL:Z15081; NID:G38501; PIDN:CA478790.1; PID:G38502
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 483; DB 2; Length 109;
Best Local Similarity 89.5%; Pred. No. 5.8e-36;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 60
DB 3 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 62

QY 61 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 63 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 107

RESULT 4
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KBA>
A/Cross-references: EMBL:X72441; NID:G443350; PIDN:CA451109.1; PID:G443351
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 88.8%; Score 482; DB 2; Length 123;
Best Local Similarity 90.4%; Pred. No. 8.1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 61
DB 20 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 79

QY 62 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 63 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105

DB 80 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 123

RESULT 5
B49047
Ig kappa chain V region (monoclonal strational autoantibody StrAB SA-1A) - human (fragme
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal strational autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <YIC>
A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.7%; Score 476; DB 2; Length 108;
Best Local Similarity 89.4%; Pred. No. 2.4e-35;
Matches 93; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 63

QY 62 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 64 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 107

RESULT 6
S31978
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31978
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977.
A/Accession: S31978
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <PDR>
A/Cross-references: EMBL:Z15074; NID:G38487; PIDN:CA478793.1; PID:G38488
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.3%; Score 474; DB 2; Length 109;
Best Local Similarity 86.7%; Pred. No. 3.6e-35;
Matches 91; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 60
DB 3 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 62

QY 61 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 63 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 107

RESULT 7
S47182
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S47182

Db 26 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKAPKLIHTTASSLSQGVPSRF 85
 QY 62 GSVSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 105
 Db 86 GSGSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 129

RESULT 12

K1HWMK Ig kappa chain precursor V-1 region (Walker) - human

C/Species: Homo sapiens (man)
 C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 21-Jan-2000
 C/Accession: A01883
 R/Klobeck, H.G.; Combratio, G.; Zachau, H.G.
 Nucleic Acids Res. 12, 6995-7006, 1984
 A/Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
 A/Reference number: A93534; MUID:85014148; PMID:6091049
 A/Accession: A01883
 A/Molecule type: DNA
 A/Residues: 1-129 <K1O>
 A/Note: the sequence was determined from the differentiated gene
 C/Genetics:
 A/Gene: GDB:IGKV1
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-22/Domain: signal sequence #status predicted <SIG>
 F/23-129/Product: Ig kappa chain V-1 region (Walker) #status predicted <MAT>
 F/23-45/Region: framework 1
 F/38-112/Domain: immunoglobulin homology <IMM>
 F/46-56/Region: complementarity-determining 1
 F/57-71/Region: framework 2
 F/72-78/Region: complementarity-determining 2
 F/79-110/Region: framework 3
 F/111-119/Region: complementarity-determining 3
 F/120-129/Region: framework 4
 F/45-110/Disulfide bonds: #status predicted

Query Match 84.3%; Score 458; DB 1; Length 129;
 Best Local Similarity 87.5%; Pred. No. 1,1e-33;
 Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKAPKLIHTTASSLSQGVPSRF 61
 Db 26 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKAPKLIHTTASSLSQGVPSRF 85
 QY 62 GSVSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 105
 Db 86 GSGSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 129

RESULT 13

K1HWMK Ig kappa chain V-1 region (Dee) - human (tentative sequence)

C/Species: Homo sapiens (man)
 C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
 C/Accession: A01865
 R/Milstein, C.P.; Devergon, E.V.
 Biochem. J. 123, 945-958, 1971
 A/Title: The amino acid sequence of a human kappa light chain.
 A/Reference number: A01865; MUID:7205133; PMID:5124396
 A/Accession: A01865
 A/Molecule type: protein
 A/Residues: 1-108 <MIL>
 A/Note: the C region of this chain as the Inv (3) marker
 C/Genetics:
 A/Gene: GDB:IGKV1
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer
 F/16-90/Domain: immunoglobulin homology <IMM>
 F/23-86/Disulfide bonds: #status predicted

Query Match 84.2%; Score 457; DB 1; Length 108;
 Best Local Similarity 84.5%; Pred. No. 1,1e-33;
 Matches 87; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKAPKLIHTTASSLSQGVPSRF 61
 Db 4 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKAPKLIHTTASSLSQGVPSRF 63
 QY 62 GSVSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 104
 Db 64 GSGSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 106

RESULT 14

S31980 Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S31980; S32000
 R/Portolano, S.; Chazebault, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 Submitted to the EMBL Data Library, June 1992
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A/Reference number: S31977
 A/Accession: S31980
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-109 <POR>
 A/Cross-references: EMBL:Z15076; NID:G38491; PTDN:CAA78785.1; PTD:G38492; EMBL:Z15083; N
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 457; DB 2; Length 109;
 Best Local Similarity 82.9%; Pred. No. 1,2e-33;
 Matches 87; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKAPKLIHTTASSLSQGVPSRF 60
 Db 3 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKAPKLIHTTASSLSQGVPSRF 62
 QY 61 GSVSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 105
 Db 63 GSGSGTDFTLTISLSLOPEDFATYYCOQSYTTPYTFGGCTKQIK 107

RESULT 15

S19674 Ig kappa chain V region (clone alpha-TEL9) - human

C/Species: Homo sapiens (man)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
 C/Accession: S19674
 R/Marke, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
 A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phi
 A/Reference number: S19663; MUID:92085276; PMID:1748994
 A/Accession: S19674
 A/Molecule type: mRNA
 A/Residues: 1-108 <MAR>
 A/Cross-references: EMBL:X61642; NID:G37860; PTDN:CAA3923.1; PTD:G1335386
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;
 Best Local Similarity 84.8%; Pred. No. 1,4e-33;
 Matches 89; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITTCRASOSIRYLNWYOHKPGAPKLLIHTASLSOSGVPSRF 60
 Db 3 VLTQSPSSLSASVGDRTVITTCRASOSISNLYNWOOKPGAPKLLIHTASLSOSGVPSRF 62
 QY 61 SGSVSGTDFTLTISLSLOPEDFATYCCQSYTTPYTFGQGTKEIK 105
 Db 63 SGSGSGTDFTLTINSLSLOPEDFATYCCQNTNSPPLTFGQGTKEIK 107

Search completed: January 22, 2004, 11:53:45
 Job time : 15.1522 secs

Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLLIHTASSLSQGVPSRFS 61
 DB 26 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLLIHTASSLSQGVPSRFS 85
 QY 62 GSVSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 105
 DB 86 GSGSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKLEIK 129

RESULT 2

KVIE_HUMAN STANDARD; PRT; 108 AA.

AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region DEE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP MEDLINE=72053133; PubMed=5124396;
 RA Miletich C.P., Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain.";
 RL Biochem. J. 123:945-958(1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01865; KIHUDE.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 49 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 88 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 7 97 FRAMEWORK-4.
 FT DOMAIN 8 107 BY SIMILARITY.
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1B51 CRC64;

Query Match 84.2%; Score 457; DB 1; Length 108;
 Best Local Similarity 84.5%; Pred. No. 2.4e-40;

Matches 87; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLLIHTASSLSQGVPSRFS 61
 DB 4 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLLIHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 104
 DB 64 GSGSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKLEIK 106

RESULT 3

KV1H_HUMAN STANDARD; PRT; 108 AA.

AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Hau.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP MEDLINE=71032830; PubMed=4097974;
 RA Matanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups.";
 RL Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PIR; A01869; KIHUDE.
 DR HSSP; P80362; IWTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.

KM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 49 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 88 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 7 97 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 83.2%; Score 452; DB 1; Length 108;
 Best Local Similarity 83.7%; Pred. No. 7.9e-40;
 Matches 87; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLLIHTASSLSQGVPSRFS 61
 DB 4 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLLIHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 105
 DB 64 GSGSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKLEIK 107

RESULT 4

KV1O_HUMAN STANDARD; PRT; 108 AA.

AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";

RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039568; PubMed=1182133;
 RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein REI refined at 2.0-A resolution.";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A91663; KIHURE.
 DR PDB; 1RE1; 17-FEB-84.
 DR PDB; 1AR2; 12-NOV-97.
 DR PDB; 1BMW; 29-DEC-99.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT STRAND 40 41
 FT STRAND 44 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT STRAND 56 57
 FT STRAND 60 61
 FT STRAND 62 67
 FT STRAND 68 69
 FT STRAND 70 75
 FT STRAND 80 82
 FT HELIX 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCEZA CRC64;
 Query Match 82.3%; Score 447; DB 1; Length 108;
 Best Local Similarity 83.5%; Pred. No. 2.6e-39;
 Matches 86; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Ig kappa chain V-I region OJ.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_Taxid=9606;
 RX [1]
 RP SEQUENCE.
 RP MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 chains";
 RL Science 169:56-59(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 DR PIR; A01872; KIHOU.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11777 MW; 8283DA42A105827E CRC64;
 Query Match 79.9%; Score 434; DB 1; Length 108;
 Best Local Similarity 73.1%; Pred. No. 5.6e-38;
 Matches 76; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SMO0406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Amyloid.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
 Query Match 79.4%; Score 431; DB 1; Length 108;
 Best Local Similarity 79.8%; Pred. No. 1.1e-37;
 Matches 83; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRLYNMYQHKRGKAPKLLIHTASSLSQGVSPRS 61
 DB 4 LTQSPSSLSASVGDRTVITCRASQSYVNYVAMPQKRGKAPKLLIHTASSLSQGVSPNFT 63
 QY 62 GSVSGTDFLTITSLQPEDPATYCCQOSYTPPYFGQGTQKIQ 105
 DB 64 GSGSGTDFLTITSLQPEDPATYCCQYNSVYTFGGGTVDIK 107
 RESULT 7
 KVI_HUMAN STANDARD; PRT; 109 AA.
 ID KVI_HUMAN
 AC P01612;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-I region Mew.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=83081018; PubMed=6816713;
 RA Bulic M., Linke R.P.;
 RT "Primary structure of the variable part of an amyloidogenic
 RT Bence-Jones Protein (Mew). An unusual insertion in the third
 RT hypervariable region of a human kappa-immunoglobulin light chain."
 RT Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
 CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
 CC ROUND.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC PIR: A01879; KIHUMV.
 DR HSSP; P80362; 1MTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SMO0406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DISULFID 23 88 BY SIMILARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 98 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 99 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11870 MW; B6ABF451SD55F5A0 CRC64;
 Query Match 79.3%; Score 430.5; DB 1; Length 109;
 Best Local Similarity 81.9%; Pred. No. 1.3e-37;
 Matches 86; Conservative 4; Mismatches 14; Indels 1; Gaps 1;
 QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRLYNMYQHKRGKAPKLLIHTASSLSQGVSPRS 61
 DB 4 MTQSPSSLSASVGDRTVITCRASQSSVDYINMYQKRGKAPKLLIHTASSLSQGVSPRS 63
 QY 62 GSVSGTDFLTITSLQPEDPATYCCQOSYTPPYFGQGTQKIQ 105
 DB 64 GSGSGTDFLTITSLQPEDPATYCCQSYNBEVTFGGGTVDIK 108
 RESULT 8
 KVI_HUMAN STANDARD; PRT; 108 AA.
 ID KVI_HUMAN
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Pule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au)."
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 CC [2]
 CC X-RAY CRYSTALLOGRAPHY.
 CC MEDLINE=77022433; PubMed=1234024;
 RA Pehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au."
 RT Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC PIR: A91653; KIHUAV.
 DR PDB; 1UV5; 30-JAN-02.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SMO0406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E801187EB6F6B9 CRC64;

Query Match 77.2%; Score 419; DB 1; Length 108;
Best Local Similarity 78.8%; Pred. No. 2e-36;

Matches 82; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYNWYQHKPKAKPKLLIHTASSLSQGVSPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITCRASQSIIRYNWYQHKPKAKPKLLIHTASSLSQGVSPSRFS 63

QY 62 GSVSGDFTLTISLSQPEDPATYTCQOSYTPPTFGGCTKQIK 105
DB 64 GSGSGTFTLTISLSQPEDPATYTCQOSYTPPTFGGCTKQIK 107

RESULT 9

KVIL_HUMAN STANDARD; PRT; 108 AA.
ID KVIL_HUMAN

AC P01603;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Ka.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=76189985; PubMed=818073;

RA Shindoda T.;

RT "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) alocypic marker."

RL J. Biochem. 77:1277-1296(1975).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01869; KIHUKA.

DR HSSP; P80362; 1MTL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003066; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 FRAMEWORK-2.

FT DOMAIN 35 49 FRAMEWORK-3.

FT DOMAIN 50 56 FRAMEWORK-4.

FT DOMAIN 57 88 FRAMEWORK-5.

FT DOMAIN 89 97 FRAMEWORK-6.

FT DOMAIN 98 107 FRAMEWORK-7.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11900 MW; 768839FBD5A2F4B CRC64;

Query Match 77.0%; Score 418; DB 1; Length 108;
Best Local Similarity 72.1%; Pred. No. 2.5e-36;

Matches 75; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

RESULT 10
KVIL_HUMAN STANDARD; PRT; 108 AA.
ID KVIL_HUMAN

AC P01611;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Wes.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=81092279; PubMed=6778806;

RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;

RT "Preparative separation of the tryptic hydrolyzate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones protein Wes)."

RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01877; KIHWS.

DR HSSP; P80362; 1MTL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003066; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 FRAMEWORK-2.

FT DOMAIN 35 49 FRAMEWORK-3.

FT DOMAIN 50 56 FRAMEWORK-4.

FT DOMAIN 57 88 FRAMEWORK-5.

FT DOMAIN 89 97 FRAMEWORK-6.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11608 MW; 782B14A69A60E45 CRC64;

Query Match 76.4%; Score 415; DB 1; Length 108;
Best Local Similarity 76.9%; Pred. No. 5e-36;

Matches 80; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYNWYQHKPKAKPKLLIHTASSLSQGVSPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITCRASQSIIRYNWYQHKPKAKPKLLIHTASSLSQGVSPSRFS 63

QY 62 GSVSGDFTLTISLSQPEDPATYTCQOSYTPPTFGGCTKQIK 105
DB 64 GSGSGTFTLTISLSQPEDPATYTCQOSYTPPTFGGCTKQIK 107

RESULT 11

KVIL_HUMAN STANDARD; PRT; 108 AA.
ID KVIL_HUMAN

AC P80362;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ig kappa chain V-I region WAT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RX MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,
 RA Solomon A., Stevens F.J., Schiffer M.,
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers.";
 RL Biochemistry 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=61267384; PubMed=6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Poppe R.A., Solomon A.,
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human ki Bence Jones protein Wac.";
 RL J. Mol. Biol. 147:185-193(1991).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003506; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KM Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT TURN 33 38
 FT STRAND 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FA697 CRC64;
 Query Match 76.1%; Score 413; DB 1; Length 108;
 Best Local Similarity 76.9%; Pred. No. 8.1e-36;
 Matches 80; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGRVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQSGVPSRFS 61
 DB 4 MTQSPSSLSASVGRVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQSGVPSRFS 63
 QY 62 GSVSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 105
 DB 64 GSGSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 107
 RESULT 12
 -KVIA_HUMAN

ID KVIA_HUMAN STANDARD; PRT; 108 AA.
 AC P01593;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-1 region AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RT complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3550-3560(1969).
 CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003506; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT TURN 33 38
 FT STRAND 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0CAF CRC64;
 Query Match 75.9%; Score 412; DB 1; Length 108;
 Best Local Similarity 77.9%; Pred. No. 1e-35;
 Matches 81; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGRVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQSGVPSRFS 61
 DB 4 MTQSPSSLSASVGRVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQSGVPSRFS 63
 QY 62 GSVSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 105
 DB 64 GSGSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 107
 RESULT 13
 -KVIA_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-1 region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=63273707; PubMed=6410398;
 RA Gont F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated

RT galactose in Klebsiella polysaccharides K30 and K33."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 DR PIR; A01876; KIHUWE.
 DR HSSP; P80362; 1WTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 75.9%; Score 412; DB 1; Length 108;
 Best Local Similarity 77.9%; Pred. No. 1e-35;
 Matches 81; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDVDTITCRASQSIIRYLWYOHKPGKAPKLLIHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDVDTITCRASQSIIRYLWYOHKPGKAPKLLIHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTITSLQPEDFATYCCQSYTTPYTFGCGTKLOIK 105
 DB 64 GSSSGTDFLTITSLQPEDFATYCCQSYTTPYTFGCGTKLOIK 107
 RESULT 14
 KVID_HUMAN STANDARD; PRT; 107 AA.
 AC P01586;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region CAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RX SEQUENCE.
 RX MEDLINE=75075135; PubMed=4216454;
 RA Milstein C.P., Deverson E.V.,
 RT "Primary structure of kappa light chain from a human myeloma
 RT protein.";
 FT Bur. J. Biochem. 49:377-391(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01864; KIHUAK.
 DR HSSP; P80362; 1WTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Glycoprotein.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;
 Query Match 75.6%; Score 410.5; DB 1; Length 107;
 Best Local Similarity 76.9%; Pred. No. 1.5e-35;
 Matches 80; Conservative 12; Mismatches 11; Indels 1; Gaps 1;
 QY 2 MTQSPSSLSASVGDVDTITCRASQSIIRYLWYOHKPGKAPKLLIHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDVDTITCRASQSIIRYLWYOHKPGKAPKLLIHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTITSLQPEDFATYCCQSYTTPYTFGCGTKLOIK 105
 DB 64 GSSSGTDFLTITSLQPEDFATYCCQSYTTPYTFGCGTKLOIK 106
 RESULT 15
 KVID_HUMAN STANDARD; PRT; 108 AA.
 AC P01604;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Kue.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RX SEQUENCE.
 RX MEDLINE=9237924; PubMed=112021;
 RA Bullitz M., Kley H.-P., Zeidler H.-U.;
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid
 RT sequence of the variable part of a human L-chain of the kappa-type.";
 RC Hoppe-Seayler's Z. Physiol. Chem. 360:725-734(1979).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01870; KIHUKU.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90EA898 CRC64;
 Query Match 75.5%; Score 410; DB 1; Length 108;
 Best Local Similarity 77.9%; Pred. No. 1.7e-35;
 Matches 81; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDVDTITCRASQSIIRYLWYOHKPGKAPKLLIHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDVDTITCRASQSIIRYLWYOHKPGKAPKLLIHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTITSLQPEDFATYCCQSYTTPYTFGCGTKLOIK 105
 DB 64 GSSSGTDFLTITSLQPEDFATYCCQSYTTPYTFGCGTKLOIK 107

Thu Jan 22 12:05:07 2004

us-09-147-443d-60.rsp

Page 8

Db 64 GSGGTEFTLINSLOPPDPATYVCOQYSRYPYFGQTKLDIK 107

Search completed: January 22, 2004, 11:51:49
Job time : 10.1304 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:42:41 ; Search time 31.5 Seconds
(without alignments)
860.175 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSLSASVGRVIT.....COQSYTPYFGQGRQLQIK 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	86.6	108	4	Q9UL77
2	458.5	84.4	107	4	Q96SA9
3	433.5	79.8	107	4	Q9UL81
4	424	78.1	108	4	Q9UL70
5	421	77.5	108	4	Q9UL79
6	389	71.6	116	4	Q96PF6
7	378	69.6	298	11	Q9QYF0
8	372	68.5	109	11	Q920E6
9	371	68.3	233	11	Q91WS9
10	370	68.1	234	11	Q8R062
11	368	67.8	234	11	Q8VCP0
12	367	67.6	234	4	Q8NEK1
13	367	67.6	234	11	Q91WF8
14	360	66.3	111	11	Q920E9
15	357	65.7	107	11	Q9ERZ9
16	357	65.7	108	4	Q9UL83

17	355.5	65.5	109	4	Q9UL78	Q9UL78 homo sapien
18	348	64.1	214	11	Q9RIAS	Q9RIAS mus musculu
19	344	63.4	108	11	Q8VITO	Q8VITO mus musculu
20	340.5	62.7	109	4	Q9UL85	Q9UL85 homo sapien
21	340.5	62.7	114	11	Q8KIF1	Q8KIF1 mus musculu
22	339.5	62.5	112	11	Q8KIF3	Q8KIF3 mus musculu
23	338.5	62.3	109	4	Q9UL86	Q9UL86 homo sapien
24	336	61.9	107	11	Q9UL84	Q9UL84 mus musculu
25	334.5	61.6	112	11	Q8KIF2	Q8KIF2 mus musculu
26	332	61.1	127	11	Q925S9	Q925S9 mus musculu
27	331.5	61.0	238	11	Q9PM37	Q9PM37 mus musculu
28	330.5	60.9	134	11	Q8VDD0	Q8VDD0 mus musculu
29	325	59.9	99	11	Q9JL74	Q9JL74 mus musculu
30	324.5	59.8	241	11	Q921A6	Q921A6 mus musculu
31	322.5	59.4	106	5	Q9J410	Q9J410 schistosoma
32	321.5	59.2	238	11	Q8VCT6	Q8VCT6 mus musculu
33	320.5	59.0	239	4	Q8NEK0	Q8NEK0 homo sapien
34	314	57.8	103	11	Q9JL80	Q9JL80 mus musculu
35	313	57.6	101	11	Q9JL78	Q9JL78 mus musculu
36	312.5	57.6	112	11	Q8KIF0	Q8KIF0 mus musculu
37	312.5	57.6	239	11	Q8VCS5	Q8VCS5 mus musculu
38	306.5	56.4	235	11	Q91W12	Q91W12 mus musculu
39	305.5	56.3	239	4	Q8TCD0	Q8TCD0 homo sapien
40	304.5	56.1	239	11	Q8KOF8	Q8KOF8 mus musculu
41	303.5	55.9	104	11	Q9JL82	Q9JL82 mus musculu
42	301	55.4	97	11	Q9JL76	Q9JL76 mus musculu
43	299	55.1	114	4	Q9UL80	Q9UL80 homo sapien
44	294	54.1	234	11	Q8R028	Q8R028 mus musculu
45	291	53.6	109	6	Q9N0W5	Q9N0W5 oryctolagus

ALIGNMENTS

RESULT 1
Q9UL77 PRELIMINARY, PRT, 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.",
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 86.6%; Score 470; DB 4; Length 108;
Best Local Similarity 87.5%; Pred. No. 3.2e-45;
Matches 91; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
2 VMTQSPSSLSASVGRVITTCRASOSIIRYLMVYQHKPGKAPLLIHTASLSQGVPSRFS 61
|||||

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Db 4 MTQSPSSLSASVGDRTVITTCRASQSISSYLNMYQOKRGPAPKLLIYAASSLQSGVPSRFS 63
QY 62 GSVSGTDFLTITISLQPEDFATYCCQOSYTPYTFGQGTQLQIK 105
Db 64 GSGSGTDFLTITISLQPEDFATYCCQOSYSTSWTFEGGTKEIK 107

RESULT 2
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE Variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igy; 1.
DR PROSITE; PS50835; Ig_Like; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B57F16 CRC64;

Query Match 84.4%; Score 458.5; DB 4; Length 107;
Best Local Similarity 88.5%; Pred. No. 6.2e-44;
Matches 92; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNMYQHKRGPAPKLLIYAASSLQSGVPSRFS 61
Db 4 MTQSPSSLSASVGDRTVITTCRASQSISSYLNMYQOKRGPAPKLLIYAASSLQSGVPSRFS 63
QY 62 GSVSGTDFLTITISLQPEDFATYCCQOSYTPYTFGQGTQLQIK 105
Db 64 GSGSGTDFLTITISLQPEDFATYCCQOSYST-LTFGGGTKEIK 106

RESULT 3
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
```

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DR EMBL; AF035033; AAD56269.1; -
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igy; 1.
DR PROSITE; PS50835; Ig_Like; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 79.8%; Score 433.5; DB 4; Length 107;
Best Local Similarity 83.7%; Pred. No. 4e-41;
Matches 87; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNMYQHKRGPAPKLLIYAASSLQSGVPSRFS 61
Db 4 MTQSPSSLSASVGDRTVITTCRASQSISSYLNMYQOKRGPAPKLLIYAASSLQSGVPSRFS 63
QY 62 GSVSGTDFLTITISLQPEDFATYCCQOSYTPYTFGQGTQLQIK 105
Db 64 GSGSGTDFLTITISLQPEDFATYCCQOSYSTA-LTFPGTKVDIR 106

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igy; 1.
DR PROSITE; PS50835; Ig_Like; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 78.1%; Score 424; DB 4; Length 108;
Best Local Similarity 80.8%; Pred. No. 4.8e-40;
Matches 84; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNMYQHKRGPAPKLLIYAASSLQSGVPSRFS 61
Db 4 MTQSPSSLSASVGDRTVITTCRASQSISSYLNMYQOKRGPAPKLLIYAASSLQSGVPSRFS 63
QY 62 GSVSGTDFLTITISLQPEDFATYCCQOSYTPYTFGQGTQLQIK 105
Db 64 GSGSGTDFLTITISLQPEDFATYCCQOSYSTA-LTFPGGTKEIK 107

RESULT 5
Q9UL79
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ID Q9UL79 PRELIMINARY; PRT; 108 AA.
 AC Q9UL79;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035035; AAD56271.1; -.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; Ig_1ike.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 108
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;
 Query Match 77.5%; Score 421; DB 4; Length 108;
 Best Local Similarity 79.0%; Pred. No. 1e-39;
 Matches 83; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
 QY 1 VMTQSPSSLSASVGDRTITCRASQSIIRYLMYQHKPGAKPLLIHTASSLSQGVPSRF 60
 DB 3 VMTQSPSSLSASVGDRTITCRASQSIIRYLMYQHKPGAKPLLIHTASSLSQGVPSRF 62
 QY 61 GSVSGTDFLTITSSLOPEDPATYCCQSTYTPYTGQTKLQIK 105
 DB 63 GSVSGTDFLTITSSLOPEDPATYCCQSTYTPYTGQTKLQIK 107
 RESULT 6
 Q96PF6 PRELIMINARY; PRT; 116 AA.
 ID Q96PF6;
 AC Q96PF6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Kappa 1 light chain variable region (Fragment).
 GN SDNK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21361171; PubMed=11468171;
 RA Comenzo R.L., Zhang Y., Martinez C., Oeman K., Herrera G.A.;
 RT "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig VL(D) germ line gene use and clonal plasma cell burden."
 RL Blood 98:714-720(2001).
 DR EMBL; AF361758; AAK51465.1; -.
 DR InterPro; IPR007110; Ig_1ike.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 116
 SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
 Query Match 71.6%; Score 389; DB 4; Length 116;
 Best Local Similarity 71.2%; Pred. No. 4.6e-36;
 Matches 74; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
 Query Match 71.6%; Score 389; DB 4; Length 116;
 Best Local Similarity 71.2%; Pred. No. 4.6e-36;
 Matches 74; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDRTITCRASQSIIRYLMYQHKPGAKPLLIHTASSLSQGVPSRF 61
 DB 4 MTQSPSSLSASVGDRTITCRASQSIIRYLMYQHKPGAKPLLIHTASSLSQGVPSRF 63
 QY 62 GSVSGTDFLTITSSLOPEDPATYCCQSTYTPYTGQTKLQIK 105
 DB 64 GSVSGTDFLTITSSLOPEDPATYCCQSTYTPYTGQTKLQIK 107
 RESULT 7
 Q90YF0 PRELIMINARY; PRT; 298 AA.
 ID Q90YF0;
 AC Q90YF0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CN 8 scfv.
 GN CN 8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Balb/c; TISSUE=Spleen;
 MEDLINE=20183931; PubMed=10706631;
 RA Shindoh N., Demura T., Fukuda H.;
 RT "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
 DR EMBL; AB036341; BAA88633.1; -.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; Ig_1ike.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 SQ SEQUENCE 298 AA; 31867 MW; E0P96B8A17004317 CRC64;
 Query Match 69.6%; Score 378; DB 11; Length 298;
 Best Local Similarity 68.3%; Pred. No. 2.6e-34;
 Matches 71; Conservative 15; Mismatches 18; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDRTITCRASQSIIRYLMYQHKPGAKPLLIHTASSLSQGVPSRF 61
 DB 176 MTQSPSSLSASVGDRTITCRASQSIIRYLMYQHKPGAKPLLIHTASSLSQGVPSRF 235
 QY 62 GSVSGTDFLTITSSLOPEDPATYCCQSTYTPYTGQTKLQIK 105
 DB 236 GSVSGTDFLTITSSLOPEDPATYCCQSTYTPYTGQTKLQIK 279
 RESULT 8
 Q920E6 PRELIMINARY; PRT; 109 AA.
 ID Q920E6;
 AC Q920E6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Plerin-mimicking anti-idiotope kappa chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20183931; PubMed=10706631;
 RA Shindoh N., Demura T., Fukuda H.;
 RT "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
 DR EMBL; AB036341; BAA88633.1; -.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; Ig_1ike.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 SQ SEQUENCE 298 AA; 31867 MW; E0P96B8A17004317 CRC64;
 Query Match 69.6%; Score 378; DB 11; Length 298;
 Best Local Similarity 68.3%; Pred. No. 2.6e-34;
 Matches 71; Conservative 15; Mismatches 18; Indels 0; Gaps 0;


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RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.:
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF- $\alpha$  monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.:
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF- $\alpha$  specific monoclonal antibody."
RL J. 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.:
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAG23804.1; -.
DR HSSP; P80362; IWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EBA6604A26C3 CRC64;

Query Match 65.7%; Score 357; DB 11; Length 107;
Best Local Similarity 62.6%; Pred. No. 1,7e-32;
Matches 67; Conservative 18; Mismatches 16; Indels 6; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITCRASQSI-----RYLNWYOHKPKGAPKLIHTASSLSQSG 55
DB 1 MTQSPSSLSASVGDRTVITCRASQSI-----RYLNWYOHKPKGAPKLIHTASSLSQSG 55
QY 56 VPSRFGSGSVSGTDFTLTITSSIQPEDFATYYCOQSYTTPYTFGQGTKL 102
DB 61 VPDHFMGSGGTDFTLTITSSVQTEDLADYFCQCHRTPTFTFGSGTKL 107

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Search completed: January 22, 2004, 11:53:12
 Job time : 35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:37:35 ; Search time 32.8696 Seconds
(without alignments)
507.043 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSLSASVGRVTIT.....CQGSYTPPYFGQTKLQIK 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	100.0	105	AAW52241	Antibody LD1/2-6-3
2	532	98.0	105	AAW52243	Antibody LD1/2-6-3
3	491	90.4	107	AAW52260	Anti-HIV gp120 imm
4	491	90.4	107	AAW01283	VL region of HIV n
5	491	90.4	107	AAW5135	Anti-gp120 antibod
6	491	90.4	107	AAW5135	Anti-gp120 antibod
7	488	89.9	111	AAW5135	Amino acid sequenc
8	488	89.9	111	AAW5135	Hepatitis C virus
9	488	89.9	240	AAW5135	Hepatitis C virus

10	488	89.9	299	22	AAW52241	Amino acid sequenc
11	487	89.7	107	22	AAW52241	Human anti-Rh(D) c
12	487	89.7	107	22	AAW52241	Human anti-Rh(D) a
13	487	89.7	107	22	AAW52241	Amino acid sequenc
14	487	89.7	107	22	AAW52241	Amino acid sequenc
15	483	89.0	105	19	AAW52217	Anti-HIV gp120 imm
16	483	89.0	107	15	AAW52217	VL region of HIV n
17	483	89.0	107	17	AAW01284	Anti-gp120 antibod
18	483	89.0	107	21	AAW52245	Anti-gp120 antibod
19	483	89.0	107	21	AAW52245	Human anti-tumour
20	483	89.0	132	18	AAW28842	Human anti-Rh(D) a
21	482	88.8	107	22	AAW52243	Human anti-Rh(D) a
22	482	88.8	107	22	AAW52243	HSA antibody relat
23	482	88.8	108	24	ABP96009	Light chain #1 for
24	482	88.8	114	18	AAW13922	A single chain ant
25	482	88.8	240	20	AAW02472	Human MUC-1 scfv c
26	482	88.8	240	22	AAW46005	Human MUC-1 scfv c
27	482	88.8	240	22	AAW46007	Human MUC-1 scfv c
28	482	88.8	240	22	AAW46008	Human MUC-1 scfv c
29	482	88.8	240	22	AAW46008	Human TF anti-idio
30	482	88.8	240	22	AAW46038	Human serum albumi
31	482	88.8	240	24	ABP95997	Human anti-Rh(D) c
32	481	88.6	107	22	AAW93601	Human anti-Rh(D) c
33	480.5	88.5	108	22	AAW93589	Human anti-Rh(D) c
34	480.5	88.5	108	22	AAW93600	Human anti-Rh(D) c
35	480	88.4	107	18	AAW16649	Anti-cancer specif
36	480	88.4	107	22	AAW93594	Human anti-Rh(D) c
37	480	88.4	108	24	AAW16706	Human anti-blood c
38	479	88.2	107	22	AAW93667	Human anti-Rh(D) a
39	479	88.2	108	24	AAW5210	Human Ige scfv 1C2
40	477	87.8	104	15	AAW54318	Anti-HIV gp120 imm
41	477	87.8	104	17	AAW01285	VL region of HIV n
42	477	87.8	104	21	AAW5137	Anti-gp120 antibod
43	477	87.8	104	21	AAW98246	Anti-gp120 antibod
44	477	87.8	108	24	AAW16708	Human anti-blood c
45	476.5	87.8	108	22	AAW93655	Human anti-Rh(D) a

ALIGNMENTS

RESULT 1	AAW52241	standard; protein; 105 AA.
ID	AAW52241	
AC	AAW52241	
DT	12-JUN-1998	(first entry)
DE	Antibody LD1/2-6-3-VL chain sequence.	
XX	Antibody, variable heavy chain; VH chain; variable light chain; VL chain;	
KW	Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;	
KM	idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.	
OS	Homo sapiens.	
XX	WO9749809-A1.	
XX	31-DEC-1997.	
PD	20-JUN-1997.	97WO-EP03253.
PF	24-JUN-1996.	96EP-0810421.
PR	(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.	
PA	Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;	
XX	Vogel M;	
PI	WPI; 1998-077173/07.	
DR	N-PSDB; AAW19765.	
DR		
XX		

PT New Rheus D antigen binding poly:peptide(s) - used to neutralise
 PT Rheus D antigen in therapy, e.g. for treating idiopathic
 PT thrombocytopenic purpura

PS Claim 1; Fig 15B; 68bp; English.

CC This sequence is the antibody LD1/2-6-3-VL chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rheus D antigens which
 CC include Rheus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rheus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rheus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rheus negative women before or immediately after the birth
 CC of a Rheus positive child to prevent haemolytic disease of the newborn
 CC (HDN) in subsequent pregnancies. In addition, anti-Rheus D
 CC immunoglobulin can be used after mistransfusions of Rheus positive blood
 CC to Rheus negative recipients in order to prevent sensitisation to the
 CC Rheus D antigen. The products can also be used as diagnostic reagents.

SO Sequence 105 AA;

Query Match 100.0%; Score 543; DB 19; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-34;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKGKAPKLLHTASSLSQGVSRF 60

DB 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKGKAPKLLHTASSLSQGVSRF 60

OY 61 SGSVSGTDFLTITSSLOPEDFATYCCOQSYTPYFGQGTQLQIK 105
 DB 61 SGSVSGTDFLTITSSLOPEDFATYCCOQSYTPYFGQGTQLQIK 105

RESULT 2
 ID AAW52243 standard; Protein; 105 AA.

XX AAW52243;

DT 12-JUN-1998 (first entry)

DE Antibody LD1/2-6-3-VL chain sequence.

KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain;

KM Rheus D antigen; anti-Rheus D immunoglobulin; HDN; therapy;

XX Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

OS Homo sapiens.

FN WO9749809-A1.

PD 31-DEC-1997.

PE 20-JUN-1997; 97WO-EP03253.

PR 24-JUN-1996; 96EP-0810421.

PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

PI Ametutz H, Imboden M, Miescher S, Morell A, Stadler B,

DR WPI; 1998-071173/07.

DR N-PSDB; AAV19767.

PT New Rheus D antigen binding poly:peptide(s) - used to neutralise

PT Rheus D antigen in therapy, e.g. for treating idiopathic

PT thrombocytopenic purpura

PS Claim 1; Fig 16B; 68bp; English.

XX This sequence is the antibody LD1/2-6-3-VL chain sequence, which is a

CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rheus D antigens which
 CC include Rheus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rheus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rheus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rheus negative women before or immediately after the birth
 CC of a Rheus positive child to prevent haemolytic disease of the newborn
 CC (HDN) in subsequent pregnancies. In addition, anti-Rheus D
 CC immunoglobulin can be used after mistransfusions of Rheus positive blood
 CC to Rheus negative recipients in order to prevent sensitisation to the
 CC Rheus D antigen. The products can also be used as diagnostic reagents.

SO Sequence 105 AA;

Query Match 98.0%; Score 532; DB 19; Length 105;
 Best Local Similarity 98.1%; Pred. No. 2.7e-33;
 Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKGKAPKLLHTASSLSQGVSRF 60

DB 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKGKAPKLLHTASSLSQGVSRF 60

OY 61 SGSVSGTDFLTITSSLOPEDFATYCCOQSYTPYFGQGTQLQIK 105
 DB 61 SGSVSGTDFLTITSSLOPEDFATYCCOQSYTPYFGQGTQLQIK 105

RESULT 3
 ID AAR54260 standard; protein; 107 AA.

XX AAR54260;

DT 25-MAR-2003 (updated)

DT 10-NOV-1994 (first entry)

DE Anti-HIV gp120 immunoglobulin light chain variable region b22.

KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

KM neutralisation; monoclonal antibody; kappa light chain;

XX variable region; framework; complementarity determining region.

OS Homo sapiens.

FN Key

FT Location/Qualifiers

FT 1..21

FT /label= FR1

FT Region

FT 22..33

FT /label= CDRI

FT Region

FT 34..48

FT /label= FR2

FT Region

FT 49..55

FT /label= CDR2

FT Region

FT 56..87

FT /label= FR3

FT Region

FT 88..95

FT /label= CDR3

FT Region

FT 96..107

FT /label= FR4

FT Region

XX WO9407922-A1.

XX 14-APR-1994.

XX 30-SEP-1993; 93WO-US09328.

XX 30-SEP-1992; 92US-0954148.

XX (SCRI) SCRIPPS RES INST.

XX	11-JUL-1995;	95MO-US08743.
PF		
XX	18-JUL-1994;	94US-0276852.
PR		
XX	(SCRI) SCRIPPS RES INST.	
PA		
XX	Barbas CF, Burton DR, Lerner RA;	
PI		
XX	WPI; 1996-179601/18.	
DR		
XX	Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in	
PT	passive immuno:therapy and detection of HIV infection.	
XX		
PS	Example; Fig 11, 366pp; English.	
XX		
CC	The sequences given in AAW01261-92 represent the light chain variable	
CC	regions (VL) of a series of monoclonal antibodies (MAb's) which are	
CC	immunoreactive with HIV glycoprotein gp120 and are capable of	
CC	neutralising HIV. This sequence represents the sequence of the Jk2	
CC	gene clones, b22 and B35. A MAb containing this VL sequence has the	
CC	capacity to reduce HIV infectivity titre in an in vivo virus	
CC	infectivity assay by 50 % at a concentration of less than 700 ng	
CC	of antibody/ml, and binds mature gp120 preferentially over the	
CC	precursor gp160. The MAb may be used for determining immunocompetence	
CC	of a human anti-HIV antibody and in the detection of HIV infection.	
XX		
SQ	Sequence 107 AA;	
	Query Match 90.4%; Score 491; DB 17; Length 107;	
	Best Local Similarity 91.3%; Pred. No. 3.5e-30;	
	Matches 99; Conservative 4; Mismatches 5; Indels 0; Gaps 0;	
QY	2 MTGSPSSLSASVGDRTVTTCRASQSITIRYINWYQHKGKAPKLIIHTASSLQSGVPSRFS 61	
Dd	2 LTGSPSSLASVDRTVTTCRASQSISSTYNWYQOKPKGAKILLIYAASSLQSGVPSRFS 61	
QY	62 GSVSQDFTLTITSLQPEDPATYYCOOSYTTPTFGGTQLTK 105	
Dd	62 GSGSGDTFTLTITSLQPEDPATYYCOOSYSTPYPFGGTLEIK 105	
	RESULT 5	
ID	AAV95135 standard; Protein; 107 AA.	
XX	AAV95135;	
AC	AAV95135;	
XX		
DT	30-JUN-2000 (first entry)	
XX		
DE	Anti-gp120 antibody light chain variable region from clone b22.	
XX		
KM	Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;	
KW	reduce HIV infection; diagnosis: immunotherapy; HIV induced disease;	
XX	glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.	
OS	Homo sapiens.	
XX		
PN	AU9948756-A.	
XX		
PD	17-FEB-2000.	
XX		
PP	16-SEP-1999; 99AU-0048756.	
XX		
PR	16-SEP-1999; 99AU-0048756.	
XX		
PA	(SCRI) SCRIPPS RES INST.	
XX		
PI	Burton DR, Barbas CF, Lerner RA;	
XX		
DR	WPI; 2000-293393/26.	
XX		
XX	Novel human monoclonal antibodies which immunoreact with and neutralise	

PT human immunodeficiency virus useful for treating HIV infections -
PS Example 9; Figure 11; 366pp; English.
XX
XX
CC The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50% at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV.
XX
SQ Sequence 107 AA;
Query Match 90.4%; Score 491; DB 21; Length 107;
Best Local Similarity 91.3%; Pred. No. 3.5e-30;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 MTGSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKKLIIHTASLSGVSRRFS 61
DB 2 LTQSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKKLIIHTASLSGVSRRFS 61
QY 62 GSVSGTDFLTITISSLOPEDFATYVCCQSYTPPTFGGTGLQIK 105
DB 62 GSGSGTDFLTITISSLOPEDFATYVCCQSYTPPTFGGTGLQIK 105
RESULT 6
ID AAY98244 standard; Protein; 107 AA.
XX
XX AAY98244;
XX
XX 04-JUL-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX passive immunotherapy; reduce severity; HIV-induced disease;
XX immunocompetence; active immunisation.
XX
XX Homo sapiens.
XX
XX AU9948754-A.
XX
XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-0048754.
XX
XX 16-SEP-1999; 99AU-0048754.
XX
XX 16-SEP-1999; 99AU-0048754.
XX
XX (SCRI) SCRIPPS RES INST.
XX

PI Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-246867/22.
XX
XX
XX Human neutralising monoclonal antibodies to human immunodeficiency
XX virus (HIV) used for providing passive immunotherapy to HIV are
XX specific for glycoprotein-120 -
XX
PS Example 9; Figure 11; 374pp; English.
XX
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
XX capable of reducing an HIV infectivity titre in an in vitro virus
XX infectivity assay by 50% at a concentration of less than 70 ng/ml. The
XX method for the production of the antibody comprises:
XX (a) providing a first polynucleotide encoding a heavy chain
XX immunoglobulin amino acid sequence (which does not comprise the sequence
XX represented by AAY98206) and a second polynucleotide encoding a light
XX chain immunoglobulin amino acid sequence;
XX (b) inserting the first and second polynucleotide sequences into a host
XX cell;
XX (c) maintaining the host cell in conditions which allow the amino acid
XX sequences encoded by the polynucleotides to be expressed in the host
XX cell; and
XX (d) isolating the antibody comprising the heavy and light chain
XX immunoglobulin amino acid sequences from the host cell.
XX The anti-HIV gp-120 monoclonal antibody is used for providing passive
XX immunotherapy to HIV in a human. They can be administered to high-risk
XX patients to reduce the likelihood and/or severity of HIV-induced disease
XX and to patients who are already HIV-infected. The antibodies are used
XX for neutralising field isolates which provides information about the
XX immunocompetence of an immune response in HIV patients, for detecting
XX HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX producing anti-idiotypic antibodies which can be used for active
XX immunisation and to screen human monoclonal antibodies to identify those
XX with the same binding specificity and to monitor the course of HIV
XX disease therapy by measuring the changes in concentration of HIV present
XX in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX monoclonal antibodies are encoded by a human polynucleotide sequence and
XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX reduce the problems of significant host immune response to the
XX antibodies associated with monoclonal antibodies of xenogeneic or
XX chimeric derivation.
XX
SQ Sequence 107 AA;
Query Match 90.4%; Score 491; DB 21; Length 107;
Best Local Similarity 91.3%; Pred. No. 3.5e-30;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 MTGSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKKLIIHTASLSGVSRRFS 61
DB 2 LTQSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKKLIIHTASLSGVSRRFS 61
QY 62 GSVSGTDFLTITISSLOPEDFATYVCCQSYTPPTFGGTGLQIK 105
DB 62 GSGSGTDFLTITISSLOPEDFATYVCCQSYTPPTFGGTGLQIK 105
RESULT 7
ID AAG63656 standard; Protein; 111 AA.
XX
XX AAG63656;
XX
XX 29-OCT-2001 (first entry)
XX
XX Amino acid sequence of the L chain variable region of ScFv3-4.
XX
XX Complementarity determining region; CDR, single chain antibody; ScFv;
XX hepatitis C virus; HCV; HCV infection; CDR1; E2 protein; NS1 protein;
XX envelope glycoprotein.
XX

XX Homo sapiens.
 OS
 XX
 XX WO200158459-A1.
 PN
 XX
 PD 16-AUG-2001.
 XX
 PF 13-FEB-2001; 2001WO-JP00967.
 XX
 PR 14-FEB-2000; 2000JP-0034906.
 XX
 XX (MITS-) MITSUBISHI-TOKYO PHARM INC.
 PA
 PI Itami S, Shibui T, Seki M, Yotsunoto Y, Matsuura Y, Miyamura T;
 XX
 DR WPI; 2001-496986/54.
 XX
 DR N-PSDB; AAH74685.
 XX
 XX Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 PT glycoprotein or CD81 -
 XX
 XX Claim 27; Page 116; 138pp; Japanese.
 PS
 CC The present sequence represents the L chain variable region of a single
 CC chain antibody of the invention. The specification describes a substance
 CC can inhibit the binding between hepatitis C virus (HCV) and cells with
 CC potential HCV infection, cells with expression of CD81, or CD81. This
 CC substance is especially an antibody with affinity towards HCV E2/NS1
 CC protein, containing amino acid sequences based on the complementarity
 CC determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable
 CC regions. The antibody inhibits the viral envelope glycoprotein. It is
 CC also a CD81 inhibitor. The antibodies and drugs are used for treatment
 CC and/or prevention of hepatitis C, or for diagnosis of hepatitis C.
 CC
 SQ Sequence 111 AA;
 XX
 XX Query Match 89.9%; Score 488; DB 22; Length 111;
 XX Best Local Similarity 89.5%; Pred. No. 6.1e-30;
 XX Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 XX
 QY 1 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNMYOHKPKAPKLIHTASLSQGVPSRF 60
 DB 3 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNMYOHKPKAPKLIHTASLSQGVPSRF 62
 QY 61 SGSVSGTDFLTITSSLOPEDFATYYCOQSYTYPTFGQGTKEIK 105
 DB 63 SGSVSGTDFLTITSSLOPEDFATYYCOQSYTYPTFGQGTKEIK 107
 XX
 XX RESULT 8
 XX ID ABJ38615 standard; Protein; 111 AA.
 XX AC ABJ38615;
 XX
 XX 12-JUN-2003 (first entry)
 XX
 XX Hepatitis C virus treatment related human protein sequence SEQ ID No 29.
 DE
 XX
 XX Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
 KM antibody; recombinant; antiviral; infection; human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003014728-A1.
 PN
 XX
 PD 20-FEB-2003.
 XX
 XX 09-AUG-2002; 2002WO-JP08175.
 PF
 XX
 PR 10-AUG-2001; 2001JP-0243947.
 XX
 XX

XX
 XX (MITS-) MITSUBISHI PHARMA CORP.
 PA
 XX (NINA-) JAPAN AGENCY NAT INST HEALTH.
 XX
 XX
 XX Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
 XX
 DR WPI; 2003-248334/24.
 XX
 XX
 XX Pharmaceutical compositions for hepatitis C containing screened
 PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
 PT antibody, useful in preventing or treating HCV infections -
 XX
 XX Example 4; Page 84; 136pp; Japanese.
 PS
 CC The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance; and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC sequence represents a human protein relating to the novel HCV therapy
 CC method of the invention.
 CC
 SQ Sequence 111 AA;
 XX
 XX Query Match 89.9%; Score 488; DB 24; Length 111;
 XX Best Local Similarity 89.5%; Pred. No. 6.1e-30;
 XX Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 XX
 QY 1 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNMYOHKPKAPKLIHTASLSQGVPSRF 60
 DB 3 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNMYOHKPKAPKLIHTASLSQGVPSRF 62
 QY 61 SGSVSGTDFLTITSSLOPEDFATYYCOQSYTYPTFGQGTKEIK 105
 DB 63 SGSVSGTDFLTITSSLOPEDFATYYCOQSYTYPTFGQGTKEIK 107
 XX
 XX RESULT 9
 XX ID ABJ38595 standard; Protein; 240 AA.
 XX AC ABJ38595;
 XX
 XX 12-JUN-2003 (first entry)
 XX
 XX Hepatitis C virus treatment related human protein sequence SEQ ID No 4.
 DE
 XX
 XX Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
 KM antibody; recombinant; antiviral; infection; human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003014728-A1.
 PN
 XX
 PD 20-FEB-2003.
 XX
 XX 09-AUG-2002; 2002WO-JP08175.
 PF
 XX
 PR 10-AUG-2001; 2001JP-0243947.
 XX
 XX (MITS-) MITSUBISHI PHARMA CORP.
 PA
 XX (NINA-) JAPAN AGENCY NAT INST HEALTH.
 XX
 XX Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
 XX
 DR WPI; 2003-248334/24.
 XX
 XX
 XX Pharmaceutical compositions for hepatitis C containing screened
 PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
 PT antibody, useful in preventing or treating HCV infections -
 XX

XX Claim 1, Page 64-65; 136pp; Japanese.

CC The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance; and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC sequence represents a human protein relating to the novel HCV therapy
 CC method of the invention.

XX Sequence 240 AA;

Query Match 89.9%; Score 488; DB 24; Length 240;
 Best Local Similarity 89.5%; Pred. No. 1.2e-29;
 Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 60
 DB 23 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 82
 QY 61 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 105
 DB 83 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 127

RESULT 10
 AAG63660
 ID AAG63660 standard; Protein; 299 AA.

XX AAG63660;
 AC
 XX 29-OCT-2001 (first entry)
 DT
 XX Amino acid sequence of single chain antibody ScFv3-4.

DE Complementarity determining region; CDR, single chain antibody; ScFv;
 KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
 KM envelope glycoprotein.
 XX Homo sapiens.
 OS
 XX MO200158459-A1.
 PN
 XX 16-AUG-2001.
 PD
 XX 13-FEB-2001; 2001MO-JP00967.
 PE
 XX 14-FEB-2000; 2000JP-0034906.
 PR
 XX (MITS-) MITSUBISHI-TOKYO PHARM INC.
 PA
 XX Itami S, Shibui T, Seki M, Yocumoto Y, Matsuura Y, Miyamura T;
 PI
 XX WPI; 2001-496986/54.
 DR
 XX N-PSDB; AAH74689.

PT Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 PT glycoprotein or CD81 -
 PT
 XX
 XX Disclosure; Page 127-129; 138pp; Japanese.

CC The present sequence represents a single chain antibody of the invention.
 CC The specification describes a substance can inhibit the binding between
 CC hepatitis C virus (HCV) and cells with potential HCV infection, cells
 CC with expression of CD81, or CD81. This substance is especially an
 CC antibody with affinity towards HCV E2/NS1 protein, containing amino acid
 CC sequences based on the complementarity determining region (CDR) 1, CDR2

CC and CDR3 of the H and L chain variable regions. The antibody inhibits
 CC the viral envelope glycoprotein. It is also a CD81 inhibitor. The
 CC antibodies and drugs are used for treatment and/or prevention of
 CC hepatitis C, or for diagnosis of hepatitis C.

XX Sequence 299 AA;

Query Match 89.9%; Score 488; DB 22; Length 299;
 Best Local Similarity 89.5%; Pred. No. 1.5e-29;
 Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 60
 DB 168 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 227
 QY 61 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 105
 DB 228 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 272

RESULT 11
 AAG93593
 ID AAG93593 standard; Protein; 107 AA.

XX AAG93593;
 AC
 XX 14-SEP-2001 (first entry)
 DT
 XX Human anti-Rh(D) chain 105 protein sequence.

DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX Homo sapiens.
 OS
 XX US6255455-B1.
 PN
 XX 03-JUL-2001.
 PD
 XX 29-JAN-1999; 99US-0240274.
 PE
 XX 11-OCT-1996; 96US-0028550.
 PR
 XX 10-APR-1998; 98US-0081380.
 PR
 XX 27-JUN-1997; 97US-0884045.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 PI
 XX WPI; 2001-388931/41.
 DR
 XX N-PSDB; AAH68650.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 PT
 XX
 XX Claim 1; Column 44; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein.
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93659. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.

XX Sequence 107 AA;
 QY Query Match 89.7%; Score 487; DB 22; Length 107;

Best Local Similarity 90.4%; Pred. No. 7e-30;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKLIHTASSLSQGVPSRF 61
Db 3 LTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKLIHTASSLSQGVPSRF 62
QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTLEIK 105
Db 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTLEIK 106

RESULT 12

ID AAG93644 standard; Protein; 107 AA.
XX AAG93644;
AC AAG93644;
XX 14-SBP-2001 (first entry)
XX Human anti-Rh(D) antibody clone SH13 protein sequence.
DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW Red blood cell; Rh phenotype; diagnosis; therapeutic.
XX Homo sapiens.
XX US6255455-B1.
XX 03-JUL-2001.
XX 29-JAN-1999; 99US-0240274.
XX 11-OCT-1996; 96US-0028550.
PR 10-APR-1998; 98US-0081380.
PR 27-JUN-1997; 97US-0884045.
XX (UYPE-) UNIV PENNSYLVANIA.
XX PA
XX Siesel DL;
PI WPI; 2001-388931/41.
DR N-PSDB; AAH68701.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX Claim 1; Column 68; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification
CC of the present invention.
XX Sequence 107 AA;

Query Match 89.7%; Score 487; DB 22; Length 107;
Best Local Similarity 90.4%; Pred. No. 7e-30;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKLIHTASSLSQGVPSRF 61
Db 3 LTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKLIHTASSLSQGVPSRF 62
QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTLEIK 105

Db 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTLEIK 106

RESULT 13

ID AAG65567 standard; protein; 107 AA.
XX AAG65567;
AC AAG65567;
XX 30-NOV-2001 (first entry)
DT Amino acid sequence of protein seq Id No. 92.
XX Gene library; immunoglobulin; antibody library; human.
XX Homo sapiens.
XX WO200162907-A1.
XX 30-AUG-2001.
PF 22-FEB-2001; 2001WO-1P01298.
XX 22-FEB-2000; 2000JP-0050543.
XX (MED-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX WPI; 2001-565420/63.
DR N-PSDB; AAH47731.
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions -
XX Examples; p 167-168; 181pp; Japanese.
XX The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries.
XX Sequence 107 AA;

Query Match 89.7%; Score 487; DB 22; Length 107;
Best Local Similarity 90.5%; Pred. No. 7e-30;
Matches 95; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 WMTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKLIHTASSLSQGVPSRF 60
Db 3 WMTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKLIHTASSLSQGVPSRF 62
QY 61 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTLEIK 105
Db 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTLEIK 107

RESULT 14

AAG65563
ID AAG65563 standard; protein; 114 AA.

AC AAG65563;
XX 30-NOV-2001 (first entry)
DT Amino acid sequence of protein seq Id No. 88.

XX Gene library; immunoglobulin; antibody library; human.
KM Homo sapiens.
OS WO200162907-A1.
PN 30-AUG-2001.
XX 22-FEB-2001; 2001WO-JP01298.
PF 22-FEB-2000; 2000JP-0050543.
XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,
PI Okuno Y, Shiraki K;
XX WPI; 2001-565420/63.
DR N-PSDB; AAH47727.
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions -
XX Examples; p 162-163; 181pp; Japanese.
PS The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries.
XX
SQ Sequence 114 AA;
Query Match 89.7%; Score 487; DB 22; Length 114;
Best Local Similarity 90.5%; Pred. No. 7.4e-30;
Matches 95; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKPGKAPKLLIHRTASLSQGVPSRF 60
DB 3 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKPGKAPKLLIHRTASLSQGVPSRF 62
QY 61 SSVSVSGTDFTLTISLQPEDFATYYCOQSYTTPYTFGGGTQLQIK 105
DB 63 SSVSVSGTDFTLTISLQPEDFATYYCOQSYTTPYTFGGGTQLQIK 107
RESULT 15
AAW52217
ID AAW52217 standard; Protein; 105 AA.
XX AAW52217;
AC
XX 12-JUN-1998 (first entry)
DT
XX
XX Antibody LD1-84-VL chain sequence.
DE
XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX Homo sapiens.
OS
XX W09749809-A1.
PN
XX 31-DEC-1997.
PD
XX 20-JUN-1997; 97WO-EP03253.
PF
XX

PR 24-JUN-1996; 96EP-0810421.
XX (ROTK-) ROTKREUTZSTIFTUNG ZENT LAB BLUTSPENDE.
PA Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
XX Vogel M;
PI
XX WPI; 1998-077173/07.
DR N-PSDB; AAV19741.
XX
XX New Rhesus D antigen binding polypeptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
XX
PS Claim 1; Fig 3B; 68pp; English.
XX
XX This sequence is the antibody LD1-84-VL chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after transfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 105 AA;
Query Match 89.0%; Score 483; DB 19; Length 105;
Best Local Similarity 87.6%; Pred. No. 1.4e-29;
Matches 92; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKPGKAPKLLIHRTASLSQGVPSRF 60
DB 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKPGKAPKLLIHRTASLSQGVPSRF 60
QY 61 SSVSVSGTDFTLTISLQPEDFATYYCOQSYTTPYTFGGGTQLQIK 105
DB 61 SSVSVSGTDFTLTISLQPEDFATYYCOQSYRBFTEGRTSLDIK 105
Search completed: January 22, 2004, 11:51:22
Job time : 34.8696 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:53:16 ; Search time 31.5 Seconds
(Without alignments)
689.122 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSISASVGRVTIT.....CQGSYTPYFGQGTMLQIK 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Published Applications AA:*
- 2: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	90.4	107	12	US-10-016-986-104
2	488	89.9	111	12	US-10-203-754A-57
3	487	89.7	107	11	US-09-848-798-36
4	487	89.7	107	11	US-09-848-798-156
5	486	89.5	107	11	US-09-791-153A-67
6	483	89.0	107	12	US-10-016-986-105
7	482	88.8	107	11	US-09-848-798-175
8	482	88.8	107	11	US-09-848-798-176
9	482	88.8	240	9	US-09-192-854-2
10	482	88.8	240	10	US-09-968-561A-2
11	482	88.8	240	12	US-09-968-744A-2
12	481	88.6	107	11	US-09-848-798-44
13	480.5	88.5	108	11	US-09-848-798-32
14	480.5	88.5	108	11	US-09-848-798-43
15	480	88.4	107	11	US-09-848-798-37

16	479	88.2	107	11	US-09-848-798-179	Sequence 179, App
17	477	87.8	104	12	US-10-016-986-106	Sequence 106, App
18	476.5	87.8	108	11	US-09-848-798-167	Sequence 167, App
19	476	87.7	111	12	US-10-203-754A-56	Sequence 56, Appl
20	474	87.3	107	12	US-10-016-986-103	Sequence 103, Appl
21	473	87.1	107	11	US-09-848-798-33	Sequence 33, Appl
22	472	86.9	107	11	US-09-848-798-38	Sequence 38, Appl
23	472	86.9	107	11	US-09-848-798-39	Sequence 39, Appl
24	471	86.7	106	12	US-10-377-121-5	Sequence 5, Appl
25	471	86.7	107	11	US-09-848-798-158	Sequence 158, App
26	469	86.4	214	15	US-10-153-382-19	Sequence 19, Appl
27	468	86.2	108	14	US-10-025-687-8	Sequence 8, Appl
28	468	86.2	108	15	US-10-125-687-8	Sequence 8, Appl
29	466.5	85.9	108	11	US-09-848-798-181	Sequence 181, App
30	466	85.8	107	11	US-09-848-798-35	Sequence 35, Appl
31	465	85.6	107	11	US-09-848-798-173	Sequence 173, App
32	465	85.6	109	12	US-10-330-613-10	Sequence 10, Appl
33	465	85.6	109	12	US-10-330-530-10	Sequence 10, Appl
34	463.5	85.4	108	11	US-09-848-798-41	Sequence 41, Appl
35	463.5	85.4	250	11	US-09-880-748-1174	Sequence 1174, Ap
36	463	85.3	127	15	US-10-283-349-71	Sequence 71, Appl
37	462	85.1	107	11	US-09-848-798-168	Sequence 168, App
38	461.5	85.0	108	11	US-09-848-798-163	Sequence 163, App
39	461	84.9	106	8	US-08-844-215-13	Sequence 13, Appl
40	461	84.9	107	11	US-09-848-798-40	Sequence 40, Appl
41	460	84.7	237	11	US-09-880-748-1906	Sequence 1906, Ap
42	460	84.7	237	11	US-09-880-748-2003	Sequence 2003, Ap
43	460	84.7	237	11	US-09-880-748-2005	Sequence 2005, Ap
44	460	84.7	237	11	US-09-880-748-2017	Sequence 2017, Ap
45	460	84.7	237	11	US-09-880-748-2019	Sequence 2019, Ap

ALIGNMENTS

```

RESULT 1
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R.
; APPLICANT: Barbas, Carlos F.
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match          90.4%; Score 491; DB 12; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.2e-38;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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QY 2 MTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 61
Db 2 LTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 61
QY 62 GSVSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 105
Db 62 GSGSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 105

RESULT 2

US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOSHIMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-754A-57

Query Match 89.9%; Score 488; DB 12; Length 111;
Best Local Similarity 89.5%; Pred. No. 1.4e-37;
Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 60
Db 3 LTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 62
QY 61 GSVSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 105
Db 63 GSGSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 107

RESULT 3

US-09-848-798-36
; Sequence 36, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 105
US-09-848-798-36

Query Match 89.7%; Score 487; DB 11; Length 107;
Best Local Similarity 90.4%; Pred. No. 1.7e-37;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 61
Db 3 LTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 62
QY 62 GSVSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 105
Db 63 GSGSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 106

RESULT 4

US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match 89.7%; Score 487; DB 11; Length 107;
Best Local Similarity 90.4%; Pred. No. 1.7e-37;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 61
Db 3 LTQSPSSLSASVGDRTYITTCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLSGVSRSRFS 62
QY 62 GSVSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 105
Db 63 GSGSGTDFLTITISLQPEDPATYCCOQSYTTPYTFGQGTLEIK 106

RESULT 5

US-09-791-153A-67
; Sequence 67, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deebande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-67

Query Match 89.5%; Score 486; DB 11; Length 107;
Best Local Similarity 90.4%; Pred. No. 2.1e-37;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 63

QY 62 GSVSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 105
DB 64 GSGSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 107

RESULT 6
US-10-016-986-105
Sequence 105, Application US/10016986
Publication No. US20030187247A1
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
FILE REFERENCE: 313.2CON1
CURRENT APPLICATION NUMBER: US/10/016.986
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/149,898
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: US 08/899,575
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 08/276,852
PRIOR FILING DATE: 1994-07-18
PRIOR APPLICATION NUMBER: US 08/178,302
PRIOR FILING DATE: 1994-01-06
PRIOR APPLICATION NUMBER: PCT/US93/09328
PRIOR FILING DATE: 1993-09-30
PRIOR APPLICATION NUMBER: US 07/954,148
PRIOR FILING DATE: 1992-09-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 105
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-016-986-105.

Query Match 89.0%; Score 483; DB 12; Length 107;
Best Local Similarity 90.4%; Pred. No. 3.9e-37;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 2 LTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61

QY 62 GSVSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 105
DB 62 GSGSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 105

RESULT 7
US-09-848-798-175
Sequence 175, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 175
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match 88.8%; Score 482; DB 11; Length 107;
Best Local Similarity 88.5%; Pred. No. 4.8e-37;
Matches 92; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 3 LTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 106

RESULT 8
US-09-848-798-176
Sequence 176, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: SORTING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match 88.8%; Score 482; DB 11; Length 107;
Best Local Similarity 88.5%; Pred. No. 4.8e-37;
Matches 92; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 3 LTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYCCQSYTTPYTFGGTKLQIK 106

RESULT 9
US-09-192-854-2
Sequence 2, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides

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FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-2

Query Match      88.8%; Score 482; DB 9; Length 240;
Best Local Similarity 90.4%; Pred. No. 1,1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
DB 136 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 195
62 GSVSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 105
196 GSGSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 239

RESULT 10
US-09-968-561A-2
Sequence 2, Application US/09968561A
Patent No. US2002016462A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match      88.8%; Score 482; DB 10; Length 240;
Best Local Similarity 90.4%; Pred. No. 1,1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
DB 136 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 195
62 GSVSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 105
196 GSGSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 239

RESULT 11
US-09-968-744A-2
Sequence 2, Application US/09968744A
Publication No. US20030148372A1
GENERAL INFORMATION:
```

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APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073
CURRENT APPLICATION NUMBER: US/09/968,744A
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-744A-2

Query Match      88.8%; Score 482; DB 12; Length 240;
Best Local Similarity 90.4%; Pred. No. 1,1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
DB 136 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 195
62 GSVSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 105
196 GSGSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 239

RESULT 12
US-09-848-798-44
Sequence 44, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 113
US-09-848-798-44

Query Match      88.6%; Score 481; DB 11; Length 107;
Best Local Similarity 89.4%; Pred. No. 5,9e-37;
Matches 93; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
DB 3 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLWYQHKPKAPKLLIHTASSLSQGVSPSRFS 62
62 GSVSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 105
63 GSGSGTDFLTITSSLSQPEDFATYCCQSYTTPYFGQGTQIK 106
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RESULT 13
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match 88.5%; Score 480.5; DB 11; Length 108;
Best Local Similarity 90.5%; Pred. No. 6,7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTYITTCRASOSIIRYLNWYQHKPKAPKLLIHTASSLSGVSRRFS 61
DB 3 LTQSPSSLSASVGDRTYITTCRASOSISYLNWYQHKPKAPKLLIHTASSLSGVSRRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYYCOQSYTTPYTFGQGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYYCOQSYTTPYTFGQGTKLQIK 107

RESULT 14
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match 88.5%; Score 480.5; DB 11; Length 108;
Best Local Similarity 90.5%; Pred. No. 6,7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTYITTCRASOSIIRYLNWYQHKPKAPKLLIHTASSLSGVSRRFS 61
DB 3 LTQSPSSLSASVGDRTYITTCRASOSISYLNWYQHKPKAPKLLIHTASSLSGVSRRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYYCOQSYTTPYTFGQGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYYCOQSYTTPYTFGQGTKLQIK 107

RESULT 15
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match 88.4%; Score 480; DB 11; Length 107;
Best Local Similarity 89.4%; Pred. No. 7,3e-37;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTYITTCRASOSIIRYLNWYQHKPKAPKLLIHTASSLSGVSRRFS 61
DB 3 LTQSPSSLSASVGDRTYITTCRASOSISYLNWYQHKPKAPKLLIHTASSLSGVSRRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYYCOQSYTTPYTFGQGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYYCOQSYTTPYTFGQGTKLQIK 106

Search completed: January 22, 2004, 12:00:42
Job time : 32.5 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:50:06 ; Search time 12.7826 Seconds
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347.553 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSLSASVGDRTIT.....CQOSYTPYFGQGLQIK 105

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491	90.4	107	1 US-08-276-852-104	Sequence 104, App
2	491	90.4	107	1 US-08-899-575-104	Sequence 104, App
3	491	90.4	107	1 US-08-899-575-104	Sequence 104, App
4	491	90.4	107	5 PCT-US95-08743-104	Sequence 104, App
5	487	89.7	107	3 US-09-240-274-36	Sequence 36, App
6	487	89.7	107	3 US-09-240-274-156	Sequence 156, App
7	483	89.0	107	1 US-08-276-852-105	Sequence 105, App
8	483	89.0	107	1 US-08-899-575-105	Sequence 105, App
9	483	89.0	107	1 US-08-899-575-105	Sequence 105, App
10	483	89.0	107	5 PCT-US95-08743-105	Sequence 105, App
11	482	88.8	107	3 US-09-240-274-175	Sequence 175, App
12	482	88.8	107	3 US-09-240-274-176	Sequence 176, App
13	480.5	88.5	108	3 US-09-240-274-44	Sequence 44, App
14	480.5	88.5	108	3 US-09-240-274-32	Sequence 32, App
15	480.5	88.5	108	3 US-09-240-274-32	Sequence 43, App
16	480	88.4	107	3 US-09-240-274-37	Sequence 37, App
17	479	88.2	107	3 US-09-240-274-179	Sequence 179, App
18	477	87.8	104	1 US-08-276-852-106	Sequence 106, App
19	477	87.8	104	1 US-08-899-575-106	Sequence 106, App
20	477	87.8	104	1 US-08-899-575-106	Sequence 106, App
21	477	87.8	104	5 PCT-US95-08743-106	Sequence 106, App
22	476.5	87.8	108	3 US-09-240-274-167	Sequence 167, App
23	476	87.7	108	2 US-08-276-852-103	Sequence 29, App
24	474	87.3	107	1 US-08-276-852-103	Sequence 103, App
25	474	87.3	107	1 US-08-899-575-103	Sequence 103, App
26	474	87.3	107	1 US-08-899-575-103	Sequence 103, App
27	474	87.3	107	5 PCT-US95-08743-103	Sequence 103, App

28	473	87.1	107	3 US-09-240-274-33	Sequence 33, App
29	472	86.9	107	3 US-09-240-274-38	Sequence 38, App
30	472	86.9	107	3 US-09-240-274-39	Sequence 39, App
31	471	86.7	107	3 US-09-240-274-158	Sequence 158, App
32	471	86.7	108	4 US-09-025-7698-14	Sequence 14, App
33	468	86.2	109	4 US-09-025-7698-28	Sequence 28, App
34	468	86.2	109	4 US-09-025-7698-43	Sequence 43, App
35	467	86.0	109	1 US-08-300-386A-43	Sequence 69, App
36	467	86.0	109	3 US-08-931-645-69	Sequence 69, App
37	467	86.0	109	5 PCT-US95-11235-69	Sequence 69, App
38	466.5	85.9	108	3 US-09-240-274-181	Sequence 181, App
39	466	85.8	107	3 US-09-240-274-35	Sequence 35, App
40	465	85.6	107	1 US-08-300-386A-66	Sequence 66, App
41	465	85.6	107	3 US-08-931-645-66	Sequence 66, App
42	465	85.6	107	3 US-09-240-274-173	Sequence 173, App
43	465	85.6	107	5 PCT-US95-11235-66	Sequence 66, App
44	464	85.5	109	3 US-09-157-370-3	Sequence 41, App
45	463.5	85.4	108	3 US-09-240-274-41	Sequence 41, App

ALIGNMENTS

RESULT 1
US-08-276-852-104
; Sequence 104, Application US/08276852

; Patent No. 5652138

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; CORRESPONDENCE ADDRESS:

; ADDRESSER: The Scripps Research Institute, Office of

; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/276,852

; FILING DATE: 18-JUL-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/954,148

; FILING DATE: 30-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 104:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-276-852-104

Query Match 90.4%; Score 491; DB 1; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDVVTTCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
DB 2 LTGSPSSLSASVGDVVTTCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61

QY 62 GSVSGTDFLTITSLQPEDFATYYCQOSYSTPTPTFGGQTKLQIK 105
DB 62 GSGSGTDFLTITSLQPEDFATYYCQOSYSTPTPTFGGQTKLEIK 105

RESULT 2
US-08-899-575-104
Sequence 104, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbias, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-104

Query Match 90.4%; Score 491; DB 1; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDVVTTCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
DB 2 LTGSPSSLSASVGDVVTTCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61

QY 62 GSVSGTDFLTITSLQPEDFATYYCQOSYSTPTPTFGGQTKLQIK 105
DB 62 GSGSGTDFLTITSLQPEDFATYYCQOSYSTPTPTFGGQTKLEIK 105

RESULT 3
US-08-899-575-104
Sequence 104, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbias, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-104

Query Match 90.4%; Score 491; DB 1; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDVVTTCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
DB 2 LTGSPSSLSASVGDVVTTCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61

QY 62 GSVSGTDFLTITSLQPEDFATYYCQOSYSTPTPTFGGQTKLQIK 105
DB 62 GSGSGTDFLTITSLQPEDFATYYCQOSYSTPTPTFGGQTKLEIK 105

RESULT 4
PCT-US95-08743-104
Sequence 104, Application PC/TUS9508743

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GENERAL INFORMATION:
APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-104

Query Match      90.4%; Score 491; DB 5; Length 107;
Best Local Similarity 91.3%; Pred. No. 7,7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Query
2 MTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKRGKAPKLLITASSLQSGVPSRFS 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 LTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKRGKAPKLLIYAASSLQSGVPSRFS 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Query
62 GSVSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 105
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 GSGSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLVEIK 105
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-09-240-274-36
Sequence 36, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: anti-Rh(D) chain 105
US-09-240-274-36

Query Match      89.7%; Score 487; DB 3; Length 107;
Best Local Similarity 90.4%; Pred. No. 1,7e-36;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Query
2 MTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKRGKAPKLLITASSLQSGVPSRFS 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 LTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKRGKAPKLLIYAASSLQSGVPSRFS 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Query
62 GSVSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 105
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GSGSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLVEIK 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 6
US-09-240-274-156
Sequence 156, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 156
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match      89.7%; Score 487; DB 3; Length 107;
Best Local Similarity 90.4%; Pred. No. 1,7e-36;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Query
2 MTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKRGKAPKLLITASSLQSGVPSRFS 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 LTQSPSSLSASVGRVTITCRASQSIIRYLNWYQHKRGKAPKLLIYAASSLQSGVPSRFS 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Query
62 GSVSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 105
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GSGSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLVEIK 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-08-276-852-105
Sequence 105, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbos, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
```

```

APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-105

Query Match      89.0%; Score 483; DB 1; Length 107;
Best Local Similarity 90.4%; Pred. No. 3,9e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0.

Cy      2  MTQSPSSISASVSGRVITTCRASQSIIRYLNWYQHHPKAPKLIIHTASSIQSGVPSRFS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2  LTQSPSSISASVSGRVITTCRASQSISSYLWYQOKPKAPKLIIHTASSIQSGVPSRFS 61
      62  GSGGTDFTLTITSSLOPEDFATYYCOQSITTPYTGQTKLQIK 105
      62  GSGGTDFTLTITSSLOPEDFATYYCOQSISTPQTGQTKLEIK 105

RESULT 8
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSSEE: The Scripps Research Institute, Office of
ADDRESSSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937

```

```

TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match      89.0%; Score 483; DB 1; Length 107;
Best Local Similarity 90.4%; Pred. No.3,9e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps

QY      2 MTQSPSSLSASVGDRTVTTCRASQSITIRYLNNYOHKPGAKPLLIHTTASSLSQGVPSSRRS 61
       :|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db      2 LTQSPSSLASVGDRTVTTCRASQSISILNMYQQKPGAPKLIIYAASSLSQGVPSSRRS 61
       |||||

62 GSVSQTDFLTITISSLPEDFAIYYCQGSYTTPYTFGGTKLQIK 105
62 GSSGTDFTLTITSLQPEDFAIYYCQGSYSTPQTFGGTKEIK 105

RESULT 9
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Flitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

```



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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 113
US-09-240-274-44

Query Match      88.6%; Score 481; DB 3; Length 107;
Best Local Similarity 89.4%; Pred. No. 5.9e-36;
Matches 93; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNMWYOHKPKAKPLIHTASSLSQGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNMWYOHKPKAKPLIHTASSLSQGVPSRFS 62
   |||||||FTLTITSSLOPEDPATYCCQSYTTPYTFGGQTKLQIK 105
63 GSGSGTDFTLTITSSLOPEDPATYCCQSYTTPYTFGGQTKLEIK 106

RESULT 14
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-32

Query Match      88.5%; Score 480.5; DB 3; Length 108;
Best Local Similarity 90.5%; Pred. No. 6.6e-36;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNMWYOHKPKAKPLIHTASSLSQGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNMWYOHKPKAKPLIHTASSLSQGVPSRFS 62
   |||||||FTLTITSSLOPEDPATYCCQSYTTPYTFGGQTKLQIK 105
63 GSGSGTDFTLTITSSLOPEDPATYCCQSYTTPYTFGGQTKLEIK 107

RESULT 15
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
```

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; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 112
US-09-240-274-43

Query Match      88.5%; Score 480.5; DB 3; Length 108;
Best Local Similarity 90.5%; Pred. No. 6.6e-36;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNMWYOHKPKAKPLIHTASSLSQGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNMWYOHKPKAKPLIHTASSLSQGVPSRFS 62
   |||||||FTLTITSSLOPEDPATYCCQSYTTPYTFGGQTKLQIK 105
63 GSGSGTDFTLTITSSLOPEDPATYCCQSYTTPYTFGGQTKLEIK 107
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Search completed: January 22, 2004, 11:54:21
Job time : 13.7826 secs

A;Molecule type: mRNA
A;Residues: 1-122 <RAA>

A;Accession: S46391
A;Status: preliminary

A;Accession: S46391
A;Status: preliminary

Query Match	71.2%;	Score 476;	DB 2;	Length 119;
Best Local Similarity	72.0%;	Pred. NO. 5.2e-37;		
Matches 90;	Conservative 14;	Mismatches 15;	Indels 6;	Gaps 1

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QY      61 GDSVYGRFTYSRDNSKNTLYIQMGLPAEDTAVYYCARAKAVGISRKNYYNDVWGKTT 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ      61 ADSVYGRFTISRDNKNTLYIQMNSLRPAEDTAVYYCARD-----KASDAFDIWGQTM 114
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

QY	121	VTVSS	125
Db	115	VTVSS	119

RESULT 15

Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31679
R:Cuisinier, A.M.; Gauchier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31679
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <CUI>
A:Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID:g30966
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:34-117//Domain: immunoglobulin homology <1MM>

Query Match	71.2%;	Score 476;	DB 2;	Length 134;
Best Local Similarity	74.4%;	Pred. No. 5.9e-37;		
Matches	93;	Conservative	9;	Mismatches 13; Indels 10; Gaps 2

OY 1 QVKTLESGGGVVQPGGSLRVACVAGFTFRNFGMHMVRQAPGKGIEMVAFLWFDASNKGY 60
 ||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 20 QVQLVESGGGVQPGSRSLRTSCAASGFPTSSYAHMWVRQAPEGKIEMAVAVISYDSNKKY 79

```

Qy      61 GDSYKGRFTYSRDNSKNTLYLQMGGLRAEDTAVYYCAREKAVRGISRYNYMDWGKTT 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80 ADSYKGRFTYSRDNSKNTLYLQMGSLRAEDTAVYYCARES--RG-----DYGQGL 129

```

QY	121	VTVSS	125
Db	130	VTVSS	134

Search completed: January 22, 2004, 11:53:44
Job time : 17.8478 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	543.5	81.2	126	3	US-09-240-274-152	Sequence 152, App1
2	543	81.2	125	3	US-09-240-274-8	Sequence 8, App1
3	543	81.2	125	3	US-09-240-274-20	Sequence 20, App1
4	543	81.2	125	3	US-09-240-274-21	Sequence 21, App1
5	543	81.2	125	3	US-09-240-274-22	Sequence 22, App1
6	542.5	81.1	126	3	US-09-240-274-17	Sequence 17, App1
7	541.5	80.9	126	3	US-09-240-274-14	Sequence 14, App1
8	541.5	80.9	126	3	US-09-240-274-15	Sequence 15, App1
9	541.5	80.9	126	3	US-09-240-274-147	Sequence 147, App1
10	541.5	80.9	126	3	US-09-240-274-148	Sequence 148, App1
11	539.5	80.6	126	3	US-09-240-274-16	Sequence 16, App1
12	535	80.0	125	3	US-09-240-274-23	Sequence 23, App1
13	533	79.7	127	3	US-09-240-274-139	Sequence 139, App1
14	530	79.2	127	3	US-09-240-274-135	Sequence 145, App1
15	528	78.9	125	3	US-09-240-274-9	Sequence 9, App1
16	527	78.8	125	3	US-09-240-274-24	Sequence 24, App1
17	526.5	78.7	126	3	US-09-240-274-26	Sequence 26, App1
18	524	78.3	127	3	US-09-240-274-19	Sequence 19, App1
19	520.5	77.8	126	3	US-09-240-274-153	Sequence 153, App1
20	519	77.6	127	3	US-09-240-274-18	Sequence 18, App1
21	518.5	77.5	126	3	US-09-240-274-25	Sequence 25, App1
22	517.5	77.4	126	3	US-09-240-274-149	Sequence 149, App1
23	503.5	75.3	310	4	US-09-079-029-11	Sequence 11, App1
24	503	75.2	125	3	US-09-240-274-140	Sequence 140, App1
25	502.5	75.1	126	3	US-09-240-274-10	Sequence 10, App1
26	502.5	75.1	126	3	US-09-240-274-144	Sequence 144, App1
27	502.5	75.1	126	3	US-09-240-274-150	Sequence 150, App1

28	497.5	74.4	126	3	US-09-240-274-146	Sequence 146, App
29	494	73.8	127	3	US-09-240-274-11	Sequence 11, App
30	492.5	73.6	126	3	US-09-240-274-13	Sequence 13, App
31	488	72.9	119	1	US-08-331-3398A-45	Sequence 46, App
32	488	72.9	119	2	US-08-331-337B-46	Sequence 46, App
33	488	72.9	119	3	US-08-753-804A-46	Sequence 46, App
34	488	72.9	119	2	US-09-227-653-46	Sequence 46, App
35	487	72.8	121	3	US-09-202-181-4	Sequence 4, App1
36	481	71.5	142	1	US-08-305-683A-2	Sequence 2, App1
37	478	71.4	287	3	US-08-862-124-17	Sequence 17, App1
38	478	71.4	304	3	US-08-862-124-17	Sequence 14, App1
39	477	71.3	125	3	US-09-240-274-151	Sequence 151, App
40	474	70.9	120	1	US-07-942-245-55	Sequence 35, App
41	472.5	70.6	140	3	US-08-983-607-32	Sequence 32, App
42	472	70.6	249	4	US-10-039-785-53	Sequence 53, App
43	471.5	70.5	248	4	US-09-315-926A-80	Sequence 80, App
44	470	70.2	245	4	US-09-566-158A-2	Sequence 2, App1
45	469.5	70.2	243	4	US-08-918-148-76	Sequence 76, App

ALIGNMENTS

```

RESULT 1
US-09-240-274-152
; Sequence 152, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ. ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-152

Query Match      81.2%; Score 543.5; DB 3; Length 126;
Best Local Similarity 80.2%; Pred. No. 8, 4e-45;
Matches 101; Conservative 14; Mismatches 10; Indels 1; Gaps

QY      1 QVLLSSGGGVVOPGSLAVACVYASGFTTRNFGMHVWRQAPGKGLFWAFIFPDASNKG 60
       1 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EYLLSSGGGVVOPGSRSLRLSCAASGFTSRNGMHVWRQAPKGLFWAFIFPDGSKKY 60
QY      61 GDSVKSRFTYYSRNSNGTLYLQWNGLRARDTAVYVCAREKAY-RGISRNYNYVDWVGKGT 11
       61 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKSRFTIISRDNSKNTIYLQWNSLRADDTAVYVCAREKALFRLGLTRNSYGDWVGQGT 12
QY      120 TVTVSS 125
       120 ||:||||
Db      121 TVSVSS 126

RESULT 2
US-09-240-274-8
; Sequence 8, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ. ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-152

Query Match      81.2%; Score 543.5; DB 3; Length 126;
Best Local Similarity 80.2%; Pred. No. 8, 4e-45;
Matches 101; Conservative 14; Mismatches 10; Indels 1; Gaps

QY      1 QVLLSSGGGVVOPGSLAVACVYASGFTTRNFGMHVWRQAPGKGLFWAFIFPDASNKG 60
       1 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EYLLSSGGGVVOPGSRSLRLSCAASGFTSRNGMHVWRQAPKGLFWAFIFPDGSKKY 60
QY      61 GDSVKSRFTYYSRNSNGTLYLQWNGLRARDTAVYVCAREKAY-RGISRNYNYVDWVGKGT 11
       61 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKSRFTIISRDNSKNTIYLQWNSLRADDTAVYVCAREKALFRLGLTRNSYGDWVGQGT 12
QY      120 TVTVSS 125
       120 ||:||||
Db      121 TVSVSS 126

```

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Db          121 VTWSS 125

RESULT 4
US-09-240-274-21
Sequence 21, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-22

Query Match      81.2%; Score 543; DB 3; Length 125;
Best Local Similarity 80.0%; Pred. No. 9,2e-45;
Matches 100; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY    1 QVRLBEGGAVNPGGLRACVASGTFFNFPGHWRQRPKGLEVAVFIMPASNKGY 60
     :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
DB    1 EVQLLBGGGVDPGRSLRLSCVVSGETFNNYGHWRAQPKGLEVAVAIVFDGSNKTY 60
QY    61 GDSTKGFPTSRPNSKNITLYLNMGLEAEPDAAVYYCARERAVRGISRYNYMDVGKQT 120
     ||::||::||::||::||::||::||::||::||::||::||::||::||::||:
DB    61 ADSVKGFFTSRPNSKNITLYLNMGSLRAEDTAIYYCARENQIKLSRIYYFDTWGCIL 120
QY    121 VTVSS 125
     |||||
DB    121 VTVSS 125

RESULT 5
US-09-240-274-22
Sequence 22, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-22

Query Match      81.2%; Score 543; DB 3; Length 125;
Best Local Similarity 80.0%; Pred. No. 9,2e-45;
Matches 100; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
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; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L

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? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
? FILE REFERENCE: 09596-42U2
? CURRENT APPLICATION NUMBER: US/09/240,274
? EARLIER FILING DATE: 1999-01-29
? EARLIER FILING DATE: 1998-04-10
? EARLIER APPLICATION NUMBER: 60/028,550
? EARLIER FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 224
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 147
? LENGTH: 126
? TYPE: PRt
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) antibody clone SH32
? IS-09-240-274-147

```

Query March	80.9%	Score 541.5;	DB 3,	Length 126;
Best Local Similarity	81.7%	Pred. No. 1,3e-44;		
Matches 103;	Conservative 9;	Mismatches 13;	Indels 1;	Gaps 1.

Dy
1 QVKTLESQGGVVQPQGSLLRVACVAGFTFRNFGHMVRQA PGKGLMVAFTWFDASKGY 600

Dz
1 EVQLTSSGGGVQPGRSRLRLSCASKPTLLYNGMHMVRA PGKGLMVAFTWFDASKKY 600

```
Qy 61 GDSYKGRFVTSRDSNKTLLQMNHRAEDTAVVYICAREKAVR-GISRYNYMDVWGKGT 119
      |||||
Db 61 EDSYKGRFVTSRDSNKTLLQMNHRAEDTAVVYICARELSKVALSRYYYMDVWGSGT 120
      |||||
```

QY	120	TVTVSS	125
Db	121	TVTVSS	126

```

RESULT 10
US-09-240-274-148
/ Sequence 148, Application US/09240274
/ Patent No. 625545
/ GENERAL INFORMATION:
/ APPLICANT: Siegel, Donald L.
/ TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
/ TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
/ FILE REFERENCE: 09596-4202
/ CURRENT APPLICATION NUMBER: US/09/240,274
/ CURRENT FILING DATE: 1999-01-29
/ EARLIER APPLICATION NUMBER: 60/081,380
/ EARLIER FILING DATE: 1998-04-10
/ EARLIER APPLICATION NUMBER: 60/028,550
/ EARLIER FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 148
/ LENGTH: 126
/ TYPE: PR1
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) antibody clone SH37
/ US-09-240-274-148

```

Query Match 80.9%; Score 541.5; DB 3; Length 126;

Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1.

Dy QY I QVKLLESGGGVQPGGSLRVACVACSGFTFRNFGMHVRQAPBGKLEWVAFIWFDASNKGY 60
:::|||||:::|||||:
Db EVQLLESGGGVQPGGRSLRLSCAASKFTLYNGMHVRQAPBGKLEWVAFIWFDGSNKYY 60

```

Qy      61 GDSYKGRFTYTRDNSKNTLYIQMNGLRADETAVYYCAREKAVR-GISYNYNYDWMGKT 119
      |||||
Db      61 EDSYKGRFTYTRDNSKNTLYIQMNSLRADETAVYYCARELSKVALSRYYYNYDWMGGQT 120

```

Qy	120	TVTVSS	125
Db	121	TVTVSS	126

RESULT 11
US-09-240-274-16
; Sequence 16, Application US/09240274

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

CURRENT FILING DATE: 1999-01-29
 EARLIER APPLICATION NUMBER: 60/081,380
 EARLIER FILING DATE: 1998-04-10

```

; EARLIER FILING DATE: 1996-10-11
;
; NUMBER OF SEQ ID NOS: 224
;
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 16

```

```

; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
;

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OTHER INFORMATION: anti-Rh(D) chain D11
US-09-240-274-16

Query Match	80.6%;	Score 539.5;	DB 3;	Length 126;
Best Local Similarity	81.0%;	Pred. No. 2e-44;		
Matches 102;	Conservative 10;	Mismatches 13;	Indels 1;	Gaps 1;

[illegible]

```

Oy      61 GDSYKGRFTVSRDNSKNTLYLQNMGLRAEPTAVVYICAREKAVR-GISRIYNYMDVWGKGT 119
        |||||
Db      61 ADSYKGRFTVSRDNSKNTLYLQNMISLRAEDTAVVYICAREVSKKLALSRYYYMDVWGQGT 120
        |||||

```

Qy	120	TVTVSS	125
Db	121	TVTVSS	126

RESULT 12
US-09-240-274-23
Sequence 23, Application US/09240274

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

;
 ; CURRENT APPLICATION NUMBER: US/09/240,219
 ;
 ; CURRENT FILING DATE: 1999-01-29
 ;
 ; EARLIER APPLICATION NUMBER: 60/081,380
 ;
 ; EARLIER FILING DATE: 1998-04-10
 ;

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; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0

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; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens

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OTHER INFORMATION: anti-Rh(D) chain dise
US-09-240-274-23

Query Match	80.0%;	Score 535;	DB 3;	Length 125;
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